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RESULT COVERS OF THE PROPERTY 
RAX MEDLINE=20195000; runweq=10/31136;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dddson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
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Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                wielsen J., Nielsen F.C., Christiansen J.; "Cloning and Expression of a Drosophila Homolog of IMP/Vg1-RBP."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. [7]
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                                                                                FlyBase; FBgn0030235; Imp. GO; GO:0003676; F:nucleic acid binding; IEA.
                                InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                            Stapleton M.,
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Search completed: July 23, 2004, 11:15:00 Job time: 120.039 secs

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SUMMARIES

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## ALIGNMENTS

TITLE	AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AR171867	RESULT 1
and Old,L,J. Isolated nucleic acid molecule encoding cancer associated antigen, the antigen itself, and uses thereof	<pre>L (bases 1 to 3283) Chen,YT., Gure,A., Tsang,S., Stockert,E., Jager,E., Alexander,K.</pre>	Unclassified.	Unknown.	Unknown.		AR171867.1 GI:17910817	AR171867	54.	AR171867 3283 bp DNA linear PAT 17-DEC-2001		

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Chen, Y.-T., Gure, A., Tsang, S., and Old, L.J.
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GAGAAGCTAAGCGGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCCGGAT
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                                       ACAGAAACCGCCGTTGTCAACGTCACATATGCAACAAGAGAAGAAGAAAAAAATAGCCATG
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                              Isolated nucleic acid molecules encoding cancer-associated antigens, these antigens and method of using the same antigens, these antigens and method of using the same antigens; these antigens and method of using the same LUDWIG INSTITUTE FOR CANCER RESEARCH

OS Homo sapiens (human)

PN JP 2002512049-A/6

PD 23-APR-2002

PF 16-MAR-1999 JP 2000545030

PF 16-MAR-1999 US 09/061709

PI 7APR-1998 US 09/061709

PI 7APR-1998 US 09/061709

PI 7AGER, ALICANDIC CHEN,ALI GURE, SOLAM TSANG, ELISABETH STOCKERT, EI JAGER,

PO C12N15/09,A61K35/12,A61K39/00,A61K39/39,A61P35/00,C07K16/PC C12N15/09,A61K35/12,A61K39/00,A61K39/39,A61P35/00,C07K16/PC C12N15/09,A61K35/12,A61K39/00,A61K39/39,A61P35/00,C07K16/PC C12N1/15
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                            GCAGAGAAGCCTGTCACCATCCATGCCACCCCAGAGGGGGACTTCTGAAGCATGCCGCATG
                                               GCAGAGAAGCCTGTCACCATCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGCATG
                                                                                                    AACATCACTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAACTCTGGAGCT
                                                                                                                                                            ATCCTGGTCCCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAG
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1023 ATACAACCCGGAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCCTGTGCCAGTGCTGA	Query Match 99.1%; Score 3253.8; DB 9; Length 3667; Best Local Similarity 99.8%; Pred. No. 0; Db
963 GAAAATTGAACATGAAACAGGGACCAAGATAACAATCTCATCTTTGGAGGATTTGAGCAT	TQAVGALIGKKGAHIKQLARFAGASIKIAPAEGPDVSERMVIITGPPEAQFKAQGRIF GKLKEENFFNPKEEVKLEAHIKVPSSTAGRVIGKGKTVNELQNLTSAEVIVPRDQTP DENEEVIVRIIGHFFASQTAQRKIREIVQQVKQQEQKYPQGVASQRSK"  Db
903 AAICTTGGCACACAATGGCTTGGTTGGAAGACTGATTGGAAAAGAAGGAGCAGAAATTTGAA 	SSPSPPQRAQROHSSREQGHAPCGTSQARQIDFPLRIIVPTQFVGAIIGKEGLTIKN ITKQTQSRVDIHRKENSGAAEKPVTIHATPEGTSEACRMILEIMQKEADETGLAEEIP LKILAHNGLVGALIGKEGRNLKKIEHETGTKITISSLQDLSITVNEGTTITVKGTVEBAC ASAEIEIMKKLREAFENDMLAVNTHSGYFSSLYPHHQFGPFPHHHSYPEQBIVNLFIP
843 TCTTGAAATCATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTGAA 	/db_xref="GI:4883681" Qy /translation="mmnklyignlspavtaddlrqlegdrklplagqvllksgyafvd YPDQWAAIRALETLSGKVELHGKIMEVDYSVSKKLRSRKIQIRNIPPHLQWEVLDGLL AQYGTVENVEQVNTDTETAVVNVTYATREEAKIAMEKLSGHQFENVSFKISYIPDEEV Db
783 AGAGAAGCCTGTCACCATCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGCATGAT	/note="RNA-binding protein" Qy /codon_start=1 /product="hepatocellular carcinoma autoantigen" pb /protein_id="AAD31596.1" pb
723 CATCACTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAACTCTGGAGCTGC	Gene 1. 3667 Qy /gene="p62" Db /gene="p62" Db
663 CCTGGTCCCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGCCTTGACCATAAAGAA	ce 1 /org / mol / db_ / db_
603 GCAAGGCCACGCCCCTGGGGGCACTTCTCAGGCCAGACAGA	ES
543 AGAGGTGAGCTCCCCTTCGCCCCCTCAGCGAGCCCAGCGGTGGGGACCACTCTTCCCGGGA	
483 GAAGCTAAGCGGGCATCAGTITGAGAACTACTCCTTGAAGATTTCCTACATCCCGGATGA	
423 AGAAACCGCCGTTGTCAACGTCACATATGCAACAAGAGAAGAAGCAAAAATAGCCATGGA	Eukaryota; Metazoa; Chordata; Cra Mammalia; Eutheria; Primates; Cat CE 1 (bases 1 to 3667) RS Zhang, J.Y., Chan, E.K., Peng, X.X.
363 GGATGGACTTTTGGCTCAATATGGGACAGTGGAGAATGTGGAACAAGTCAACACAGACAC 	ens (human)
	ION Homo sapiens complete cds ON AF057352
243 CTCGGGTAAAGTGGAATTGCATGGGAAAICATGGAAGTTGATTACTCAGTCTCTAAAAA 	T 4
183 CGGCTACGCCTTCGTGGACTACCCCGACCAGAACTGGGCCATCCGCGCCATCGAGACCCT	QY 3241 CCNATATGGCCTTCTTTGGACAAACCTTGAAAATGTTTATTT 3283  [
	Qy 3181 GAGAAGGTGACAGTGTGCAACAGCTGTTCTGAATTGTCTTCGCTAGCCAAGAA 3240
63 GAGACGGATGAAGAAGCTTTACATCGGGAACCTGAGCCCCGCCGTCACCGCCGACGA	QY 3121 TTTTTATTTTTATTAAAAATGAGTTGGAAAAAAAATAAGATATCAACTGCCAGCCTG 3180
	QY  3061 CCTCAGCACCTTGCTCTTGTGTTTCCCTTAGAGATTTTGTAAAGCTGATAGTTGGAGCAT 3120  Db  3061 CCTCAGCACCTTGCTCTTGTGTTTCCCTTAGAGATTTTGTAAAGCTGATAGTTGGAGCAT 3120

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1 (chen,Y.-T., Gure,A., Tsang,S., Stockert,E., Jager,E., and Old,L.J.
1 solated nucleic acid molecule encoding cancer associathe antigen itself, and uses thereof patent: US 657556-A 6 10-JUN-2003;
1 patent: US 637556-A 6 10-JUN-2003;
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3232 AGCCAAGAACCNATATGGCCTTCTTTTGGACAAACCTTGAAAATGTTTATTT 3283 	3172 GCCAGCCTGGAGAAGGTGACAGTCCAAGTGTGCAACAGCTGTTCTGAATTGTCTTCCGCT 3231	3112 TTGGAGCATTTTTTTTTTTTTTTTATAAAAATGAGTTGGAAAAAAAA	3052 GIGITITIACCICAGCACCITGCICTIGIGITITCCCTIAGAGAITITIGIAAAGCIGAIAG 3111	2992 CAGGGCGTTAAATTCACAGAGTTTTTTTAACGAGAAAAACACACAGAAGAAGCTACCTCAG 3051 	2932 ATTCCTTTCTTAAAAAAAAAATGTGGAGGAAAGTAGAAATTTACCAAGGTTGTTGGCC 2991	2872 AAAGAATGTATTTTGTCTTTTTGCATTTTGGTGTATAAGCCATCAATATTCAGCAAAATG 2931	B12 AGGAAAACAGGAACCCACCAAACCAACCAACCAAACAAA	2752 CTTACACTTGGTTACTCAAAAGAACAAGAGTCAATGGTACTTGTCCTAGCGTTTTGGAAG 2811	2692       GTGCTCTGAGTATCACATCACAAAAGGAACAAAAGCGAAACACAAACCAGCCTCAA 2751	2632 TITCCTCATCCCTCCATCTCAATCCCGTATCTACGCACCCCCCCC	2572 CTCTCTGTTARCTCTCCCTCCCTCCCCTCCCCTTCTTCTCCATCTCCATCTTTTGAA 2631	TCTCTTTGCTTCACAGGTTTTAAACTGGTTTTTGCATACTGCTATATAATTCTCTGTCT		2392 CTCGTCGGAAGGACACTCACGGCAGTTCTGGATCACCTGTGTATGTCAACAGAAGGGATA 2451	332 GTCTCACGGTGTAGAGAGGAGCTTTGAGGCCACCCGCACAAAATTCACCCAGAGGGAAAT 2391	272 TTTTTCTTTTAAAGAGAAAGCAGGCTTTTCTAGACTTTAAAGAATAAAGTCTTTTGGGAG 2331	2341 TTTAGAAATAATATATCAAATAACTCAACTAACTCCAATTTTTAATCAATTATT
Qy 301 AAGCTAAGGACAGGAAAATTCAGATTCGAAACATCCCTCCTCACCTGCAGTGGAGGGGGGGG							/mol_type="genomic_DNA" /db_xref="taxon:9606"  ORIGIN	FT /organism='Homo sapiens (numan)'.  FEATURES Location/Qualifiers  source 13412  forganism="Homo sapiens"	ers	PC C12N1/15, PC C12N1/19,C12N1/21,C12N5/10,C12P21/08,C12Q1/68,G01N33/53,G01N33/ PC 574,	ER, XANDER N15/09	PN 06 200201277 PD 23-ARR-2002 PF 16-MAR-1999 JP 2000545030 PR 17-ARR-1998 US 09/061709 PR 17-ARR-1	antigens, these antigens and method of using the same JOURNAL Patent: UP 2002512049-A 4 23-APR-2002; LUDWIG INSTITUTE FOR CANCER RESEARCH COMMENT ON TO 2002512040-A/A		Homo sapiens (I Homo sapiens Eukaryota; Meta Mammalia; Euthe	ACCESSION BD209925  VERSION BD209925.1 GI:33019695  KEYWORDS JP 2002512049-A/4.	LOCUS BD209925 3412 bp DNA linear PAT 17-JUL-2003 DEFINITION Isolated nucleic acid molecules encoding cancer-associated

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                                                                                                         Homo sapiens IGF-II mRNA-binding protein MGC:29539 IMAGE:5090334), complete cds. BCC21290
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3633)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.
                                                       Homo sapiens
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                                                                    Homo sapiens
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E. J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Mitting, M., Madan, A., Rodrigues, S., Sanchez, A., Mitting, M., Madan, A., Rodrigues, S., Sanchez, A., M., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Generation and mouse cDNA secnences
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 27552765
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: nisc_mg@nhgri.nih.gov

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.M., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,

Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,

McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,

Young,A., Zhang,L.-H. and Green,B.D.
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on Aug 19, 2003 this sequence version replaced gi:18204200
Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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        GGTCCCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAGAACAT
                                                           GETGAGCTCCCCTTCGCCCCCCCAGCGAGCCAAGCGTGGGGACCACTCTTCCCGGGAGCA
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	2337 ACGGTGTAGAGAGGAGCTTTGAGGCCACCCGCACAAAATTCACCCAGAGGGAAATCTCGT 2396
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	2217 AAATAATATATCAAATAACTCAACTAACTCCAATTTTTAATCAATTATT
	2157 GATGTTAAGATATGTGGGCTGTGGGTTACACAGGGTGCCTGCAGCGGTAATATATTTTAG 2216
×	2097 GCACACCCTTTTTCTGTGGCAAATCGTCTCTGTACATGTGTGTACATATTAGAAAGGGAA 2156 
	2037 ACGACGCTATCCCTTTTAGTTGAACTAACATAGGTGAACGTGTTCAAAGCCAAGCAAAAT 2096 
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	1917 AGGGGCGGGAAGGTCAGGCAGGTTTGCCAGAACCACCGAGCCCCGCCCCCCCC
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	1797 AGAATGAGACCAAACGCAGCCAGACCAGATCGGGAGCAAACCAAAGACCATCTGAGGAATG 1856 
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	1677 ACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGCAGCAA 1736 
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RESULT 9
AC020629
LOCUS
DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM AC020629 142971 bp DNA linear PRI 07-MAR-2002 Homo sapiens 12g BAC RP11-76E16 (Roswell Park Cancer Institute Human BAC Library) complete sequence. HTG. AC020629 AC020629.6 GI:7656675

REFERENCE AUTHORS

ISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Craniata; Craniata; Vertebrata; Menac, C.,

Bunac, C., Bunac, C., Bailey, M., Baroks, A., Buhay, C., Bunac, C.,

Burkett, C., Burrows, J., Farantz, D., Ding, Y., Domah-Rashid, N.,

Duyan, Rocha, S., Durbin, K. J., Fernandez, C., Ferraguto, D.,

Duyan-Rashy, J., Frantz, P., Ganesh, R., Gorrell, J. H., Gorrell, L. L.,

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Holloway, C., Hosak, H., Issar, A., Jackson, L., Juckson, J., Liu, J., Liu, W.,

Lau, S., Leal, B., Lee, E., Li, Z., Kondejewski, N., Kong, Y., Kovar, C.,

Lozado, R. J., Lu, J., Lucier, R., Marondel, I., Martin, R.,

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Yang, R., Yu, W., Zhou, X., Kucherlapati, R., Melson, D. and

Yang, A.M., Yang Xhang,A.M., Yang,R., Yu,W., Zhou,X.,
Gibbs,R.
Direct Submission

TITLE

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Submitted (07-MAR-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Apr 27, 2000 this sequence version replaced gi:7025656. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu
                                                                                                                                                                         Direct Submission
Submitted (28-APR-2000) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA (bases 1 to 142971)
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Baylor Plaza, Houston,
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Worley, K.C.
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Baylor Plaza, Houston,
3 (bases 1 to 142971)
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                                                                                                                                                         Worley, K.C.
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Direct Submission
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are c sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing. only

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found

http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

QUALSTAT-REPORT

Number of Consensus Changing edits:	Fraction of Phrap values less than 40:	Phrap values in estimate: Average error rate (RCM_Dhrap estimate):	Contig length:	Summary Statistics
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Distribution of Quality < 40 Bases

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Query Match 85.3%;
Best Local Similarity 93.7%;
Matches 3084; Conservative C
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GCTAGCCAAGAACCNATATGGCCTTCTTTTGGACAAACCTTGAAAATGTTTA 3280 	ACTGCCAGCCTGGAGAAGGTGACAGTCCAAGTGTGCAACAGCTGTTCTGAATTGTCTTCC 3228	TAGTIGGAGCATTITITATITTITAATAAAAAIGAGTIGGAAAAAAAAAA	3050 AGGTG-TITTTACCTCAGCACCTTGCTCTTGTGTTTCCCTTAGAGATTTTGTAAAAGCTGA 3108 	CCAGGGCGTTAAATTCACAGATTTTTTTAACGAGAAAAACACAGAG-AAGAAGCTACCTC 3049 	ATTCCTTTCAAAAAAAAAATGTGGAGGAAAGTAGAAATTTA-CCAAGGTTGTTGGC 2990 	

DEFINITION ORGANISM Clark, S. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Human DNA Direct Submission AL596177.4 GI:15552942 (bases 1 to 91084 bp DNA linear PRI 08-SEP-2001 sequence from clone RP11-325P15 on chromosome 1, complete 91084)

VERSION KEYWORDS

ACCESSION

SOURCE

RESULT 10 AL596177 LOCUS

COMMENT

REFERENCE AUTHORS TITLE JOURNAL AL Submitted (08-58P-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 11, 2001 this sequence version replaced gi:15022347.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an altempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. EMBL; Sw:, SWISSEPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Groun. Purther information can be found at Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1
RP11-325P15 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm

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FEATURES
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/chromosome="1"
/clone="RP11-325P15"
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                                             ACCTGACAGAATGAGACCAAACGCAGCCAGCCAGATCGGGAGCAAACCAAAGACCATCTG
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ACCAAACAAAGAAAAAT 2                  ACCAAACAAAGAAAAAAT 1	803 177	Qy 2 Db 12
ATGGTACTTGTCCTAGCG 2802          ATGGTACATGTCCTAGCG 1217	743 117	ш.
AAAGCGAAACACACAAAC 2742                  AAAGTGAAACACACAAAAC 1211	683 057	Qy 2 Db 12
GCACC-CCCCCCCCA 26 	997	<u> </u>
TICTICTCCATCTCCATT 262	937	
GCATACTGCTATATAATT 256	504 877	μ,
ATGCCTGTCTAGCTCATA 2503	444 F 817 F	н
ACCTGTGTATGTCAACAG 2443            ACCTGTGTATGTCAACAG 1181	384 757	H .:
CGCACAAAATTCACCCAG 2383                CACACAAAATTCACCCAG 1175	324 697	H 63
AAAGAATAAAGTC 232	1637	
TTTTAATCAATTATTAAT 226               TTTTAATCAATCATTAA- 116	2209	μ,
GIGCCIGCAGCGGTAATA 220 	2149 AAAGGAAGATGTTAAGATATGTGGCCTGTGGGTTACACAGGGTGCCTGCAGCGGTAATA	Ωy 11
ACATGTGTGTACATATTAG 214                  ACATGTGTATACATATTAG 115	2089 1462	μ.
TIGAACGIGITCAAAGCCA 208                            IGAIGCGITCAAAGCCA 114	1404	
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CACCGAGCCC-CGCCTCCC 196	1910 1284	ъ.
GGCCCTGAGAATTCCAGGG 1:		Db 1

REFERENCE AUTHORS	TITLE	REFERENCE AUTHORS TITLE TOURNAL REFERENCE AUTHORS	RESULT 11 AC015706 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Qy 32 Db 126	QY 32	Qy 316 Db 1253	Qy 31 Db 124	Qy 3(	Qy 29 Db 123	Db 12:
3 (bases 1 to 182695)  Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Bowkhyalter, B., Brown, A., Burkett, G., Collins, S., Collymore, A., Coske, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FittHugh, W., Gage, D., Dagle, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,	Cooke, P., DeAreliano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., McMann, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morran, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassilev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.  Direct Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 182695)  Birren, B., Linton, L., Nusbaum, C. and Lander, E.  Homo sapiens chromosome 1, clone RP11-325915  Unpublished  2 (bases 1 to 182695)  Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,  Rrown A. Cattle A. Cattle A. Cattle, M. Cattle, N., Boukhgalter, B.,  Rrown A. Cattle, M. Cattle,	182695 bp DNA linear is chromosome 1 clone RP11-325P15 map 1, W I/ unordered pieces.  GI:8096833 GI:8096833 is (human)	280 ATTT 3283      654 ATTT 12657	220 TIGICTICCGCTAGCCAAGAACCNATAIGGCCTICITITGGACAAACCTIGAAAAIGITT 3279 	160 AAGATATCAACTGCCAGCCTGGAGAAGGTGACAGTCCAAGTGTGCAACAGCTGTTCTGAA 3219 	3101 AAAGCTGATAGTTGGAGCATTTTTTTA-TTTTTTAATAAAAAATGAGTTGGAAAAAAAA	3042 GCTACCTCAGGTG-TITTTACCTCAGCACCTIGCTCTIGTGTTTTCCCTTAGAGATTTTGT 3100	2982 GTTGTTGGCCCAGGGCGTTAAAITCACAGATTTTTTTAACGAGAAAAACACAGAGAAGAA 3041                     2354 GTTGCTGGCCCAGGGCATTAAAITTTACAGATTTTTTTAATGGGAAAAACACACAGAAAAA 12413	12297 CAGCAAAATGATTTCTTTCTTTAAAAAAAATGTGGAGGAAAGTAGAAATTTACCAAG 12353

COMMENT

Center code: WIBR Web site: http://v

JOURNAL

Direct Submission

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McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N., O'Neil,D., Olivar,T.M., Raymond,C., Riley,R., Rogov,P., Rothman,D., Disani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Doy, A. Carron B. Cohange C. Correr, D. Corner, D. Cohange C. Corner, D. Corner, D. Cohange C. Correr, D. Corner, D. Cohange C. Corner, D. Co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (24-AUG 2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 26, 2000 this sequence version replaced gi:6454072. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 141788 bases at least Q40 Consensus quality: 163541 bases at least Q30 Consensus quality: 174666 bases at least Q20 Consensus quality: 174666 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert size: 181000; agarose-fp Insert size: 181095; sum-of-contigs
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117051: gap of 100 bp
143611: contig of 26560 bp
143711: gap of 100 bp
182695: contig of 38984 bp
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32809 32909 37001 37101 45184 45284 53422 53422 53522 64477 64577

18481 18581 23094 23194 28214 28314

23093; 28213

18580 18480

28313: 32908: 37000:

120

19305 60

180 19425

19485

19365

6170 10461 10561 14301 14401

2036 2136 6070

6169:

Db 20429 CGTTC  Qy 1250 AGGCT         Db 20489 AGGCT	1130 20369 1190	Db 20249 GGATT  QY 1070 GTGCC        Db 20309 GTGCC	951 20189 1011	891 20141	Db 20021 CTCTG  Qy 831 ATGCC  Db 20081 ATGCC	711 19961 771	Qy 657 GCGGI         Db 19901 GCAGO	2y 598 C-GG Qy 598 C-GG Db 19841 CGGGG	19721 538	19666 478	418	361	Db 19486 CTCT Qy 301 AAGC Qy 19546 AAGC
GGCATCATCACTCTTATCC	TGGCTGTTAACACCCACTCCCGGATACTTCTCCAGCCTGTACCC	GAGCATAAATAACCAGGAA GTGCTGAGATAGAGATTATO 	TTTGAAGAAATTGAACAT(	TCTGAAAATCTTGGCACAC 	AGCTGCAGAGAAGCCTGTC	PAAAGAACATCACTAAGCAG	GCGGATCCTGGTCCCCACC                       GCAGGTCCTGGTCCCTACAGTTTG	AGAGGTGAGCTCCCCTTCGC AGCAAGGCCACGCCCCTGGG	aggctaagcgggcatcagt agaggtgagctccccttcgc	agaaaccactgttgtcaacg 3aagctaagcggggatcagt 	igracititegeteaatate ngaaaccgccgttgtcaacg 	TGGACTTTTGGCTCAATATG	GGGTAAAGTGGAATTGCATC
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CTTCATCCCAACCC 20488 GCTGGCGAGATTCG 1309	_ 유 - 유 - 유 - 유 -	CACAGTTTGAGGCCT 20308 TTGAAAATGATATGC 1129            TTGAAAATGATATGT 20368	AATCTCATCTTTGCA 1010 AATCTCATCTTTGCA 20248 AATCTCATCTTTGCA 20248	2014 950 2018	2008	CCATAGAAAAGAGAA 770	71	1984 656 1990	ATTTCCTACATCCCG 1978 GGGGACCACTCTTCC 597	GAAAATAGAC 1972 ATTTCCTACATCCCG 537	CAACAAGTCAACACA 1966 GAAGCAAAAATAGCC 477 	417	195
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TITEGGAAGGTCTCACGGTGTAGAGAGAGAGCTTTGAGGCCACCCGCACAAAATCACCCCAGAGCTTTGAGGCCACCCGCACAAAATTCACCCCAGAGCTTTGAGGAGAGGAGCACCCGCACAAAATTCACCCCAGAGCCCCAGAGAGCTCCACACAAAATTCACCCAGAGAAGACTCACCAAGAAATTCACCCAGAGGAAATCCACCCAGAAAATCCACCCAGAGGAAATCCACCCAGAAAATCCACCCAGAGGAAATCCACCCAGGAAAATCCACCCAGAAAATCCACCCAGAGAAATCCACCCAGGAAAATCCACGGCAAGTTCTGGAATCACCTGTGTATGTCAACAGAGAAATCTCACGGCAAGTTCTGGATCACCTGTGTATGTCAACAGAGAGAAATCACCTGTGTATGTCAACAGAGAGAAATCTCAGGGAAATCACCTGTGTATGTCAACAGAGAGAATCACCTGTGTATGTCAACAGAGAGAATCACCTGTGTATGTCAACAGAGAGAATCACCTGTGTATGTCAACAGAGAGAG	TATTTAGAAATAATATATCAAATAACTCAACTAACTCCAATTTTAATCAATTAATAA	AGCAMANIGEACACCCTITITITIGIGACAAGTCATCTCTGTACATGTGTGAAAGGGAAAAATGTTAAGATATGTGGCCTGTGGGTTACACAGGGTGCCTG	GAACTCCCACGACGCTATCCCTTTTAGTTGAACTAACATAGGTGAACGTGTTCAAAGCCA	GCCCCCAGGGCTTCTGCAGGCTTCAGCCATCCACTCACCATCCACTCGGATCTCTCCT	GCCGAGGAGGGGTCGGGAAAGGTCAGCTAGGATTTGCCAGAACCACTGGAGAATTCCAGGGGCCCGAGGAACCACCGAGGAGGTCAGGTTTTGCCAGAACCACCGAGGCCAGGTTCTCAC	ACCIGACAGAATIGAGACCAAACGCAGCCACCACCATCGGGAGCAAACGAAACGAACG	GCAGCAAGTGAGGCTCCCACAGGCACCAGCAAAACAACGGATGAATGTAGCCCTTCCAAC	AAATTGTACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCT	ACTIVANCAGIGGAGAAGTCAIGGTGCCTCGTGACCAAAGGCCAGATGAAAATGAGGAAG   TGATCGTCAGAAATTATCGGGCACTTCTTTTGCTAGCCAGACTGACAGAGCGCAAGATGAACACAGG   TGATCGTCAGAAATTATTCGGACACTTCTTTTGCTAGCCAGACTGCATAGACAGAC	CLITICLACAGCIGGCCGGGIGATIGGCAAAGGTGTCAATACCTTGAATGAACTGCAGA ACTTAACCAGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAG ACTTAACCACHIIIIIIIIIIIIIIIIIIIIIIIIIIIII	CTTTTCCACAGCTGGCCGGGTGATTGGCAAAGGTGGCAAGACCGTGAACGAAC	AAGAGGAAAACTTCTTTAACCCCAAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTG	CCACCAGCCTCCATCAAGATCGCCCTTGCGGAAGGCCCAGACGTCAACGAAAGGATGGTCA CCAGCAGCCTCCATCAAGATCGCCCTTGCGGAAGGCCCAGACGTCAACGAAAGGATGGTCA TCATCACCGGGCCACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTTGGGAAACTGA TCATCACCGGGCCACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTTGGGAAACTGA TCATCACCCGGCCACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAACTGA
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GACTITAAAAGA GCCACCCGCACA          CCACCCACACAI	CCAATTITTAA                         - CCATTITTAA ACTITAAAGAA;                     ACTITAAAGAA;	EGIACAIGIGIATAGATATAG CAGGGIGCCIGCAGCGGTAATA 	ATAGGTGAACG	ACCATCCACT	AGAGGCCCTC  AACCACCGAG                     AACCACTGGG	GEGAGCAAACC	:GGATGAATGT          :GGATGAATGG	CCTCAGGGAG	AGGCCAGAT( ACTGCACAGC	CARTACCTTG	AAGACCGTG	GCTGGAAGCG(	AGACGTCAACO

RESULT 12 AC104980 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Оу 3 Db 22	Оу 3 Дъ 22	Qy 3 рь 22	Qy 3 рь 22	Qy 3 Db 22	Qy 2. Db 22	Qy 2 Db 22	Qy 21 Db 22	Qy 21 Db 22	Qy 2 <sup>7</sup> Db 211	Qy 26 Db 219	Qy 26 Db 216	Qy 25 Db 218	Qy 25 Db 217	Qy 2444 Db 21682	Db 21622
AC104980  187226 bp DNA linear PRI 31-MAR-2002  HOMO sapiens chromosome 8, clone RP11-281D17, complete sequence.  AC104980  AC104980.5 GI:19849375  HTG.  Homo sapiens (human)	3280 ATTT 3283       2519 ATTT 22522	3220 TTGTCTTCCGCTAGCCAAGAACCNATATGGCCTTCTTTTGGACAAACCTTGAAAATGTTT 3279 	3160 AAGATATCAACTGCCAGCCTGGAGAAGGTGACAGTCCAAGTGTGCAACAGCTGTTCTGAA 3219 	3101 AAAGCTGATAGTTGGAGCATTTTTTTA-TTTTTTTAATAAAATGAGTTGGAAAAAAAA	3042 GCTACCTCAGGTG-TTTTTACCTCAGCACCTTGCTCTTGTGTTTTCCCTTAGAGATTTTGT 3100 	2982 GTTGTTGGCCCAGGGCGTTAAATTCACAGATTTTTTTAACGAGAAAAACACACAGAAGAA 3041 	2922 CAGCAAAATGATTCCTTTCTTTAAAAAAAAAATGTGGAGGAAAGTAGAAATTTACCAAG 2981                 2162 CAGCAAAATGATTTCTTTCAAAAAAAAATGTGGAGGAAAGTAGAAATTTACCAAG 22218	2863 TCCACAATGAAAGAATGTATTTTGTC-TTTTTGCATTTTGGTGTATAAGCCATCAATATT 2921 	2803 TTTTGGAAGAGGAAAAACAGGAACCCACCAAACCAATCAACCAAACAAA	2743 CAGCCTCAACTTACACTTGGTTACTCAAAAGAACAAGAGTCAATGGTACTTGTCCTAGCG 2802 	1683 GGCAAAGCAGTGCTCTGAGTATCACATCACACAAAAAGGAACAAAAGCGAAAACCACAAAAC 2742 	2624 CTTTTGAATTTCCTCATCCCTCCATCTCAATCCCGTATCTACGCACC-CCCCCCCCCC	2564 CTCTGTCTCTCTGTTTATCTCTCCCCTCCCTCCCCTCCC	2504 CACCCATITCTCTTTGCTTCACAGGTTTTAAACTGGTTTTTTGCATACTGCTATATAATT 2563	444 AAGGGATACCGTCTCGTGAAGAGGAAACTCTGTCACTCCTCATGCCTGTCTAGCTCATA 2503	
	AI	TI JC REFI						REFE AU	JO					ΑU	AU TII JOJ	REFE

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Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Ribeack, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (31-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 31, 2002 this sequence version replaced gi:19683374. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Center clone name: 281_D_17
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/mol_type="genomic DNA"
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547 GTGAGCT-CCCCTTCGCCCCCTCAGCGAGCCCAGCGTGGGGACCACTCTTCCCGGGAGCA 605
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                                                           CTAAGCGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCCGGATGAAGAG 546
                                                                                                         ACTGCTGTTGTCAATGTCACATATGCAACAAGGAAGAAGC-AAAATAGCCATGGAGGAG 79878
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                                    CTAAGCGGGCATCAGTTTGAGAACTATTCCTTCAAGATTTCCTACATCCTGGATGAAGAG
                                                                                                                                 ACCGCCGTTGTCAACGTCACATATGCAACAAGAGAAGAAGCAAAAATAGCCATGGAGAAG
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                                                                                                                                                                                                                                                                                   AGGAGCAGGAAAATTCAGATTCGAAACATCCCTCCTCACCTGCAGTGGGAGGTGTTGGAT 366
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complement(25000. .25014)

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25015. .25083
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complement(29177. .2)
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complement(15607. .159
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complement(25762...26)
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complement(17149. .17
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1625 TCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCAGGGAAATTGTACAACAGG 1684		1505 GCCGGGTGATTGGCAAAGGTGGCAAGACCGTGAACGAACTGCAGAACTTAACCAGTGCAG 1564	80707TCAAGGCCCAGGGACGGAICTICGGGAAGCTAAAAGAAGAAGAAGAAACTACT 80734  1445 TTAACCCCAAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCCACAGCTG 1504	CGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAACTGAAAGAGGAAAACTTCT		1205 ACTCTTATCCAGAGCAGGAGATTGTGAATCTCTTCATCCCAACCCAGGCTGTGGGCGCCA 1264		1086 AGAGATTATGAAGAAGCTGCGTGAGGCCTTTGAAAATGATATGCTGGCTG	CAACCCGGAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCCTGTGCCAGTGCTGAGAT	80290 GETGGCCCACAATGGCTTGTITIGIANGAACAATCTCATCTTTGCAGGATTTGAGGATATA 1025 966 AATTGAACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCATATA 1025	TGAAAGCATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCLLCIGAAAAAACTAGCCGAAGACAATTCCLLCIGAAAAAACTAGCCACAAGACAATTCCAAAAAAAAAAAA		CACTGAGCAGACCCAGTCCCGGGTAGACATCCATAGAAAAGAGAACTCTGGAGCTGCAGA GAAGCCTGTCACCATCCATGCCACCCCAGAGGGGGACTTCTGAAGCATGCCGCATGATTCT		79998 AGGTCACG-CCCTGGGGGCTCTTCTCAGGCCGGACAGACTGATTTCCCGGCTGCGGATCCA 80056 666 GGTCCCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAGAACAT 725	
Db 82005	œ	Db 81885	æ	Qy 2464 Db 81765	Db 81705		00	Qy 2104 Db 81469 Qy 2224	ω	Qy 2044 Db 81353	Qy 1984 Db 81294	Qy 1924 Db 81234	Оу 1864 Db 81175	Qy 1804 Db 81115	Qy 1744 Db 81055	Db 80935 Qy 1685 Db 80995
	GCTC	A CITCULO CONTROL CONT		AGAGGAAACTCTGTCACTCCTCATGCCTGTCTAGCTCATACACCCATTTCTCTTTGCTTC	AGACTCACGGCAGTTCTGGATCACCTGTGTATGTCAACAGAAGGGATACCGTCTCCTTGA	AGAG	ATATCAAATAACTCAACTAATTCCAAATTTTTAATCAACTATTAATTTTTT	AGAITACHOCCUCIONOCIACITO IN THE CONTROL OF THE CONT		TATCCCTTTTAGTTGAACTAACATAGGTGAACGTGTTCAAAGCCAAGCAAAATGCACACCACCAAGCAAAATGCACACCACCAAGCAAAATGCACACCACCAAGCAAG	TGCAGGCTTCAGCCATCCACTTCACCATCCACCCGGATCTCTCCTGAACTCCCACGACGC		TGCGGAGGCGGCCAGGACTCTGCCGAGGCCCTGAGAACCCCAGGGGCCGAGGAGGAGGGGCG 1923	GACCAAACGCAGCCAGATCGGGAGCCAAACCAAAGACCATCTGAGGAATGAGAAGTC 1863 	TCCCACAGGCACCAGCAAAACAAGGGATGAATGTAGCCCTTCCAACACCTGACAGAATGA 1803 	TCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAGTATCAGGGAAACTGTACAAGAGG 80994 TGAAGCAGCAGGAGCAGAATACCCTCAGGGAGTCGCCTCACAGCGCAGCAAGTGAGG-C 1743

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Strausberg,R.L., Feingold,B.A., Grouse,L.H., Derge,J.G.,

RS Strausberg,R.L., Feingold,B.A., Grouse,L.H., Schaefer,C.M., Schuler,G.D.,

RIschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Maxy,S.I., Wang,J., Hsieh,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,

Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,

Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,

McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.M.,

Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,

Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,

Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,B.D.,

Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,

Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus RIKEN cDNA C330012H03
IMAGE:5354659), partial cds.
BC023758
Contact: nisc_mgc@nhgri.nih.gov

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Blatrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,

Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,

McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,

Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (05-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903
                                                                                                                                                                                  Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGAGCA----
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                  AAGAACATCACTAAGCAGACCCAGTCCCGGGTAGACATCCACAGAAAGGAGAACTCTGGG
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/strain="FVB/N"
/db_xref="taxon:10090"
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1 (bases 1 to 2010)

Nielsen,J., Christiansen,J., Lykke-Andersen,J., Johnsen,A.H.,

Wewer,U.M. and Nielsen,F.C.

A family of insulin-like growth factor II mRNA-binding proteins represses translation in late development

Mol. Cell. Biol. 19 (2), 1262-1270 (1999)
                                                                                                                                                                                                                                                  2 (bases 1 to 2010)
2 (bases 1 to 2010)
Nielsen,J., Christiansen,J., Lykke-Andersen,J., Johnsen,A.H.,
Wewer,U.M. and Nielsen,F.C.
Direct Submission
Submitted (30-DEC-1998) Institute of Molecular Biology, University
of Copenhagen, Soelvgade 83H, Copenhagen DK-1307, Denmark
Location/Qualifiers
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/gene="IMP-2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCTGGCGGGACAGGTCCTGCTGAAGTCCGGCTACGCCTTCGTGGACTACCCCGACCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u> Accreaecceccercacceaceaecrecceceaecrecririseseaecaecaecrec</u>
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                                                                                                                                                                                                                                                                                                                                                                                                CCTTCAAGATTTCCTACATCCCGGATGAAGAGGTGAGCTCCCCTTCGCCCCCTCAGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAGAGAAGAAGCAAAAATAGCCATGGAGAAGCTAAGCGGGCATCAGTTTGAGAACTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAATGTGGAACAAGTCAACACAGACACAGAAACCGCCGTTGTCAACGTCACATATGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAATGTGGAACAAGTCAACACAGACACAGAAACCGGCGGTTGTCAAACGTCACATATGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCCTCCTCACCTGCAGTGGGAGGTGTTGGATGGACTTTTGGCTCAATATGGGACAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGAAGTTGATTACTCAGTCTCTAAAAAGCTAAGGAGCAGGAAAATTCAGATTCGAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTEGGCCATCCGCGCATCGAGACCCTCTCGGGTAAAGTGGAATTGCATGGGAAAATCA
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               CCCAGCGTGGGGACCACTCTTCCCGGGAGCAAGGCCACGCCCCTGGGGGGCACTTCTCAGG
                                                                                                                                                                                                                                                                                                   CCCAGCGTGGGGACCACTCTTCCCGGGAGCAAGGCCACGCCCCTGGGGGCACTTCTCAGG
                                                                                                                                                                                                                                                                                                                                                                 CAAGAGAAGAAGCAAAAATAGCCATGGAGAAGCTAAGCGGGCATCAGTTTGAGAACTACT
                                                                                            TCGGAAAGGACGCTTGACCATAAAGAACATCACTAAGCAGACCCAGTCCCGGGTAGATA 754
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kilahnglygrligkegrnikkviehetgtktisslodlsixndertitwgtveacpa
kaleimkklreafendmlavnqqaalifeklusalgifstgelsplagprgappa
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plyhpftmsgyfsglyghdqfgpprmviitgeppagfkaqgrifgklkeenfpnykeevk
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/protein_id="AAD09827.1"
/db_xref="GI:4191610"
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/note="binds multiple
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1765	1706 ACCCTCAGGGAGTCGCCTCACAGCGCAGCAAGTGAGGCTCCCACAGGCACCAGCAAAACA
1705 1811	1646 AGACTGCACAGCGCAAGATCAGGGAAATTGTACAACAGGTGAAGCAGGAGGAGGAGGAGTAAT
1645 1751	1586 ARACGCCAGATGAAAATGAGGAAGTGATCGTCAGAATTATCGGGCACTTCTTTGCTAGCC
1585 1691	1526 GCAAGACCGTGAACGAACTGCAGAACTTAACCAGTGCAGAAGTCATCGTGCCTCGTGACC
1525 1631	1466 AGCTGGAAGCGCATATCAGAGTGCCCTCTTCCACAGCTGGCCGGGTGATTGGCAAAGGTG
1465 1571	1406 AGGGACGGATCTTTGGGAAACTGAAAGAAGAAACTTCTTTAACCCCAAAGAAGAAGATGA
1405 1511	1346 CAGACGTCAGCGAAAGGATGGTCATCATCACCGGGCCACCGGAAGCCCAGTTCAAGGGCCC
1345 1451	1286 ACATCAAACAGCTGGCGAGATTCGCCGGAGCCTCTATCAAGATTGCCCCTGCGGAAGGCC
1285 1391	1226 TIGIGAATCICTICAICCCAACCCAGGCTGIGGGCGCCAICATCGGGAAGAAGGGGGGACAC
1225 1331	1166 TGTACCCCCATCACCAGTTTGGCCCGTTCCCGCATCACTCTTATCCAGAGCAGGAGA
1165 1271	1141
1140	1152 GCGCACTTGGCATCTTTTCAACAGGACTGTCCGTGCTATCTCCACCAGCAGGGCCCCGCG
115	92 TTGAAAATGATATGCTGGCTGTTAACCAACAAGCCAATCTG
1140	115 TTGAAAATGATATGCTGG
1114 1091	1055 GCACAGITGAGGCCTGTGCCAGTGCTGAGATAGAGATTATGAAGAAGCTGCGTGAGGCCT
1054	995 CAATCTCATCTTTGCAGGATTTGAGCATATACAACCCGGAAAGAACCATCACTGTGAAGG 
994	935 TGATTGGAAAAGAAGGCAGAAATTTGAAGAAAATTGAACATGAAACAGGGACCAAGATAA 
934	875 CCAAACTAGCCGAAGAGATTCCTCTGAAAATCTTGGCACACAATGGCTTGGTTGG
. 874	815 AGGGACTTCTGAAGCATGCCGCATGATTCTTGAAATCATGCAGAAAGAGGCAGATGAGA 
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1992 GCCGAGGCCCTGAGAACCC 2010	1886 GCCGAGGCCCTGAGAACCC 1904	1932 CGGGAGCAAACCAAAGACCATCTGAGGAATGAGAAGTCTGCGGAGGCCGCCAGGGACTCT 1991	1826 CGGGAGCAAACCAAAGACCATCTGAGGAATGAGGAAGTCTGCGGAGGCGGCCAGGGACTCT 1885	1872 ACGGATGAATGTAGCCCTTCCAACACCTGACAGAATGAGACCAAACGCAGCCAGC	1766 ACGGATGAATGTAGCCCTTCCAACACCTGACAGGAATGAGACCAAACGCAGCCAGC	1812 ACCCTCAGGGAGTCGCCTCACAGCGCAGCAAGTGAGGCTCCCCACAGGCACCAGCAAAACA 1871

Search completed: July 24, 2004, 13:04:44 Job time: 12667.7 secs

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Minimum DB
Maximum DB
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Maximum Match 100%
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## ALIGNMENTS

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XX Can 17-APR-1998; 16-MAR-1999; WO9954738-A1 Cancer associated antigen; An alternative AAZ36154; (LUDW-) 28-OCT-1999. Homo sapiens 11-FEB-2000 AAZ36154 standard; DNA; 3283 BP LUDWIG (first INST CANCER RES. 98US-00061709. 99WO-US005766 form of DNA encoding cancer associated antigen KOC-3. entry) KOC-3; cancer; vaccine; CT7;

Nucleotides representing cancer-associated products for the diagnosis, monitoring and genes, used to development of cancers develop

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WPI; 2000-013284/01.

Claim 55; Page 42-43; 44pp; English.

The present sequence represents an alternative form of a cancer associated antigen gene designated KOC-3. The specification also describes a cancer associated antigen designated CT7. The CT7 polymuclectide was isolated from SK-MEL-37 melanoma cells. The polypeptide has some homology with MAGE-10, limited to about 210 carboxy terminal amino acids. The amino terminal of the protein has a repetitive pattern, with repeats rich in serine, proline, glutamine and leucine, and an almost invariable core of the peptide given in AAY43877. The CT7 polypeptide can be processed to peptides which provoke lysis by cytolytic T cells. The polymucleotides and polypeptides can be used for treating a cancerous condition and screening for or diagnosing cancerous conditions. The cancer associated antigens can be used as an immunogenic or vaccine composition with an adjuvant, e.g. cytokine, a saponin, or granulocyte

61 AAGAGACGATTGATTGAGAACAGCTTTACATCCGGAACCCGGCCGCCGCGCGCTTGAGACCCGGCACCCGGCACAGAACTTCCGGAAACTCCCGGCACAACTCCGGAAACTCCCGGCACAAACTCCCGGCACAAACTCCCGGCACAAACTCCCGGCACAAACTCCCGGCACAAACTCCCGGCACAAACTCCCGCGCACAAACTCCCCGCCGCCGCCGCCGCCGACAAACTCCCCGGCACAAACTCCCCGCCCTGCGCGACAACTCCCCCGCCCTGCGCCACAAACTCCCCGCCCTTCCGGCACAAACTCCCCGACCAAACTCCCCCCCC	CC macrophage-colony stimulating factor (GM-CSF)  XX SQ Sequence 3283 BP; 945 A; 833 C; 779 G; 725 T; 0 U; 1 Other; SQ Sequence 3283 BP; 945 A; 833 C; 779 G; 725 T; 0 U; 1 Other;  Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 3283; Conservative 0; Mismatches 0; Indels 0; Gaps Matches 3283; Conservative 0; Mismatches 0; Indels 0; Gaps  Qy 1
141 ACCCACTCUGARIACTITICCACACCCONTICACCACTCUCACACCCCATCCCAGGACTTCTCCCACACCCCAGGACTTCTCCCACACCCCAGGCTTCCCCACACCCCAGGCTTCCCCACACCCCAGGCTTCCCCACACCCCAGGCTTCCCCACACCCCAGGCTCTCCCCACCCCAGGCTCTCCCCACCCCAGGCTCTCCCACCCCAGGCTCTCCCACCCCAGGCTCTCCCACCCCAGGCTCTCCCACCCCAGGCTCTCTCCCCCCCC	961 1021 1021 1081 1081

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210	TCTCTGTACATGTGTGTACATATTAGAAAGGGAAGATG 21 	60
16	VATATATTTTAGAAAT 22              VATATATTTTAGAAAT 22	
22	ARTATATCAAATAACTCAACTAACTCCAATTTTTAATCAATTATT	
2281 2281	TTAAAGAGAAAGCAGGCTTTTCTAGACTTTAAAGAATAAAGTCTTTGGGAGGTCTCACGG 23	
w w	TGTAGAGAGGAGCTTTGAGGCCACCCGCACAAAATTCACCCAGAGGGAAAATCTCGTCGGA 2 	
4 4	AGGACACTCACGGCAGTTCTGGATCACCTGTGTATGTCAACAGAAGGGATACCGTCTCCT 24	0 0
46	TGAAGAGGAAACTCTGTCACTCCTCI	0 0
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2581 2581	ATTTC	0 0
2641 2641	TCCCGTATCTACGCACCCCCCCCCCCCCCCCCCCCCCCC	0 0
	ACAAAAGCGAAAACACAAACCAGCTCAACTTACACTT 27 	0 0
2761 2761	CAATGGTACTTGTCCTAGCGTTTTGGAAGAG                   CAATGGTACTTGTCCTAGCGTTTTGGAAGAGA	0 0
2821	TCCACAATGAAAG <i>i</i>              TCCACAATGAAAG <i>i</i>	0 0
2881 2881	GTATAAGCCATCAATATTCAGCAAAATGATTCCTTTC 294 	0 0
29 <b>4</b> 1 29 <b>4</b> 1	IGGCCCAGGGCGTT 300 	0 0
3001	AGAAGAAGCTACCTCAGGTGTTTTTA 306	0 0
0 0	TGTTTCCCTTAGAGATTTTGTAAAGCTGATAGTTGGAGCAT 312                    TGTTTCCCTTAGAGATTTTGTAAAGCTGATAGTTGGAGCAT 312	- J
3121 3121	TTTTTTATTTTTAATAAAATGAGTTGGAAAAAAAAAAA	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB;
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23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-639362/73
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Claim 1; SEQ ID NO 6786; 103pp; English.

biodiversity.

CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polymucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC of sites expressing (II). (I) and (II) are useful in medical imaging
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications
CC polypeptide and polynucleotide sequences have applications
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity

and to recombinant produces there are markers because the produce to the produce the produce there is a produce to the produce the produce there is a produce to the produce the produce there is a produce to the produce there is a produce the produce there is a produce to the produce the produce the produce the produce the produce the produce the produce the produce the produce the produce the produce the produce the produce the produce the produce the produce the produce the produce that the produce that the produce the produ amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnost The invention relates to isolated polynucleotide (I) and polypeptide (II)

Sequence 3667 BP; 1081 A; 882 C; 846 G; 858 T; 0 U; 0 Other;

Query Match 99.1%; Score 3253.8; BB υ ••

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CTATATGGCCTTCTTTTGGACAAACCTTGAAAATGTTTATTT
               CNATATGGCCTTCTTTTGGACAAACCTTGAAAATGTTTATTT
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ABS76442 standard; cDNA; 3667

ABS76442;

11-DEC-2002 (first

encoding

human ovarian cancer marker

M452.

Human; ovarian cancer; marker; cancer; familial history; brain disordentral nervous system disorder; bacterial meningitis; viral meningi alzheimer's disease; Parkinson's disease; cerebral oedema; hydroceph brain herniation; inflammation; encephalitis; testicular disorder; nontuberculous granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm; histological type; carcinogenic; ovarian cancer marker; gene; ss. viral meningitis; ema; hydrocephalus; in disorder; meningitis;

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19-SEP-2002

14-MAR-2002; 2002WO-US007826

19-SEP-2001; 26-SEP-2001; 26-SEP-2001; 26-SEP-2001; 14-MAR-2001; 10-AUG-2001; 14-MAR-2001; ; 2001US-0276025P. 2001US-0276026P. ; 2001US-0311732P. ; 2001US-0323580P. ; 2001US-0325107P. ; 2001US-0325104P. ; 2001US-0325149P.

MILLENNIUM PHARM

RE, Ë 댭 Gannavarapu M, Hoersch S, Kama Morrisey MP, Olandt PJ, Sen A, u K, Schmandt RE, Zhao X, Glatt Glatt K; Kamatkar S, Vieby PO, Kovatis S

P-PSDB; 2002-723277/78. ABG96346.

Assessing whether a patient is afflicted with ovarian cancer, useful in assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and from a non cancer patient.

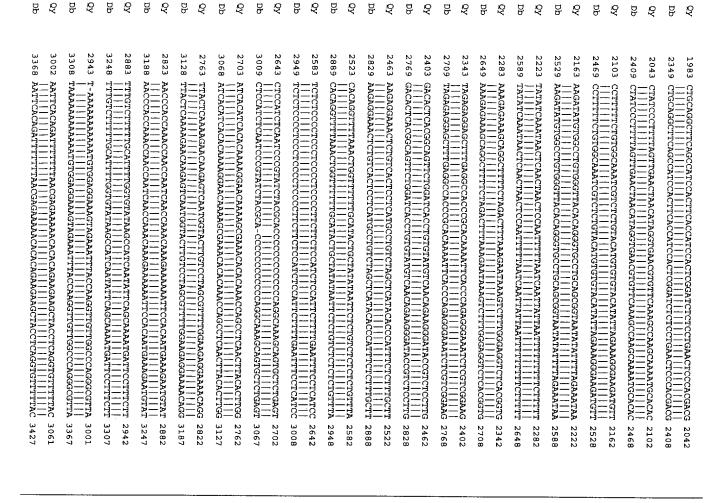
Disclosure; Page 262-263; 481pp; English

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XW I The present invention relates to a new method for assessing whether a CC patient is afflicted with ovarian cancer. The method involves comparing CC the expression level of a marker in a patient sample and the normal level CC of expression of the marker in a control non-ovarian cancer sample, where CC the marker is selected from 363 cancer markers described in the CC specification. The method of the invention is useful in diagnosing or CC characterising cancer, in detecting the presence of cancer as early as CC possible, and the recurrence of ovarian cancer. The method may also be of CC particular use with patients having an enhanced risk of developing CC ovarian cancer (e.g. patients having a familial history of ovarian concer). The cancer markers may be used in the management and treatment CC cancer). The cancer markers may be used in the management and treatment CC of e.g. brain and central nervous system disease), brain cd isorders (e.g. bacterial or viral meningitis or brain herniations), CC dinflammations (e.g. bacterial or viral meningitis or brain herniatis), testicular disorders (e.g. nontuberculous grannlomatous orchitis). testicular disorders (e.g. nontuberculous granulomatous orchitis), connective tissue disorders, or heart disorders (e.g. ischaemic heart disease or atherosclerosis). The compositions and methods may also be where level of.

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                      The present sequence represents a cancer associated antigen gene designated KNC-3. The specification also describes a cancer associated antigen designated CT7. The CT7 polynucleotide was isolated from SK-MEL-37 melanoma cells. The polypeptide has some homology with MAGE-10, limited to about 210 carboxy terminal amino acids. The amino terminal of the protein has a repetitive pattern, with repeats rich in serine, proline, glutamine and leucine, and an almost invariable core of the protein has a repetitive, and an almost invariable core of the peptide given in AAY43877. The CT7 polypeptide can be processed to peptides which provoke lysis by cytolytic T cells. The polynucleotides and polypeptides can be used for treating a cancerous condition and screening for or diagnosing cancerous conditions. The cancer associated antigens can be used as an immunogenic or vaccine composition with an adjuvant, e.g. a cytokine, a saponin, or granulocyte macrophage-colony cutimulating factor (GM-CSF)
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2000US-0231243P. 2000US-0231244P. 2000US-0231413P. 2000US-0231414P.

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The invention relates to isolated nucleic acid molecules and their concoded secreted proteins. The nucleic acids and proteins are used to grevent, treat or ameliorate a medical condition in e.g. humans, mice, crabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a gathological condition. Antibodies to the proteins can also be used in calleviating symptoms associated with the disorders and in diagnostic calleviating symptoms associated with the disorders and in diagnostic calleviating symptoms associated with the disorders and in diagnostic careful calleviating symptoms associated with the disorders and in diagnostic careful calles of the breast or liver, cardiovascular disorders e.g. cardiac neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac nerveit, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, careful system disorders e.g. cardiacy cardiacy is cardiacy viruses and fungi and ocular disorders e.g. corneal infection, bacteria, viruses and fungi and ocular disorders e.g. corneal infection, can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to capabilities, fat content, lipid, protein, carbohydrate, vitamins, capabilities, fat content, lipid, protein, carbohydrate, vitamins, capabilities, fat content, lipid, protein, carbohydrate, vitamins, capabence encodes a novel secreted protein of the invention. Note: The sequence data for this patent did not form part of the printed
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Human; gene; ds; neural disorder; immune system disorder; renal disorder muscular disorder; respiratory disease; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorde; hyperproliferative disorder; immunosuppressive; antiinflammatory; blood related disorder; cancer; immunosuppressive; antiinflammatory; cardiovascular; nephrotropic; cytostatic; antiallergic; thrombolytic; antiarteriosclerotic. system disorder; renal disorder; disorder;

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Best Local
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              GAAGGACACTCACGGCAGTTCTGGATCACCTGTGTATGTCAACAGAAGGGATACCGTCTC
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AAS26153 standard; CDNA; 2290 ВР

AAS26153

07-NOV-2001 (first entry)

CDNA encoding a novel secreted protein, Seq IJ

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                    CA,
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                                                                                                                                                                                                                                                                                                                                                                                            Matches 2028;
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives.
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P-PSDB; AAU16166.
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                                                                                                                                                TCATCATCACCGGGCCACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAAC
                                                                                                                                                                                                                                    TCGCCGGAGCCTCTATCAAGATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGG
                                                                                                                                                                                                                                                                                              CCCACGCGTCCGGCGCCATCATCGGGAAGAAGGGGGGCACACATCAAACAGCTGGCGAGAT
                                                                                                                                                                                                                                                                                                                                 CCCAGGCTGTGGGCGCCATCATCGGGAAGAAGAGGGGGCACACATCAAACAGCTGGCGAGAT
  TGAAAGAGGAAAACTTCTTTAACCCCAAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAG
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                                                                                                TCATCATCACCGGGCCACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAAAC
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AGCGCAGCAAGTGAGGCTCCCACAGGCACCAGCAAAACAACGGATGAATGTAGCCCTTCC

GGGAAATTGTACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCAC

GGGAAATTGTACAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCAC

AAGTGATCGTCAGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCA

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AAGTGATCGTCAGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCA

AGAACTTAACCAGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGG

AGAACTTAACCAGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              haemostatic;
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2000US-0214886P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorder;
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1247 CCCAGGCTGTGGGCGCATCATCGGGAAGAAGGGGGGCACACATCAAACAGCTGGCGAGAT

Query Match Best Local Sim Matches 2028;

Similarity

60.6%;

Score 1989.8; Pred. No. 0; 0; Mismatches

Conservative

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Indels Length 0 Other;

Gaps

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1306

2290 4;

Sequence

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The invention relates to human novel polypeptides and their associated CC polynucleotides. The polypeptides and polynucleotides are useful in gene therapy for treating, inhibiting or preventing neural disorders, immune CC system disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis C1 and multiple sclerosis), muscular disorders, respiratory diseases (e.g. CC nasal vestibulitis, nasal polype and sinusitis), reproductive disorders, CC (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left theart syndrome), renal disorders (e.g. acute kidney failure and end-stage CC renal disease), hyperproliferative disorders (e.g. Hodykin's disease and CC appendicitis), allergic reactions and conditions (e.g. asthma), blood CC related disorders (e.g. thrombosis, atherosclerosis and myocardial CC infarction) and cancerous diseases. Sequences ABX73173-ABX74167 represent c...
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08-DEC-
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a- 01	CCAGAGG 2386         CCAGAGG 1164	2327 GGGAGGTCTCACGGTGTAGAGAGGAGCTTTGAGGCCACCCGCACAAATTCAC
<i>"</i> — 01	AGTCTTT 2326        AGTCTTT 1104	267 ATTITTITTTTTAAAGAAAAGCAGGCTTTTCTAGACTTTAAAGAATAA 
01	ATTATTA 2266          ATTATTA 1044	2207 TATATTTTAGAAATAATATATCAAATAACTCAACTAACTA
	GCGGTAA 2206         GCGGTAA 984	AGATATGTGGCCTGTGGGTTA 
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	ATCTCTC 2026	1967 CCGCCCCCAGGGCTTCTGCAGGCTTCAGCCATCCACTTCACCATCCACTCGGACTALLINING CCGCCCCCCAGGGCTTCTGCAGGCTTCAGCCATCCACTTCAGCATCCACTCCGGACTAGGAGCTTCAGCCATCCACTCAGCATCCACTCAGCATCCACTCAGGCAGG
	CGCCTC 1966	1907 GGGGCCGAGGAGGGGGGAAGGTCAGCCAGGTTTGCCAGAACCACCGAGCCC
	ACCCCA 1906         ACCCCA 684	1847 CTGAGGAATGAGAAGTCTGCGGAGGCGGCCAGGGACTCTGCCGAGGCCCTGAGAA
	GACCAT 1846         GACCAT 624	1787 AACACCTGACAGAATGAGACCAAACGCAGCCAGACCAGA
	CCCTTCC 1786	1727 AGCGCAGCAAGTGAGGCTCCCACAGGCACCAGCAAAACAACGGATGAATGTAGC
	CCTCAC 1726	CAGGGAGTCG          CAGGGAGTCG
	\AGATCA 1666        \AGATCA 444	1607 AAGTGATCGTCAGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCA
	ATGAGG 1606       ATGAGG 384	1547 AGAACTTAACCAGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATC
	AACTGC 1546       AACTGC 324	CAAGACCGTO
	CAGAG 14       CAGAG 26	accccaagaagaagtagtgaagctggaagcgg 
	GGAAAC 1426         GGAAAC 204	1367 TCATCATCACCGGGCCACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGG
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                   TACCTCAGGTGTTTTTACCTCAGCACCTTGCTCTTGTGTTTTCCCCTTAGAGATTTTGTAAA
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                                                           TACCTCAGGTGTTTTTACCTCAGCACCTTGCTCTTGTGTTTTCCCTTAGAGATTTTGTAAA
     CTTCGGCTAGCCAAGAACCNATATGGCCTTCTTTTGGACAAACCTTGAAAATGTTTATTT
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AAS70981 standard; cDNA; 2010 BP

13-FEB-2002 (first entry)

DNA encoding novel human diagnostic protein #6785

Human; chromosome mapping; gene mapping; gene therapy; forensic;

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CC sequences. (I) is useful as hybridisation probles, to and polypeptide (II) creation (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used CC and in recombinant production of (II) for polynucleotides are also used CC in diagnostics as expressed sequence tags for identifying expressed contivity of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore normal CC activity of (II) or to treat disease states involving or quantitating a CC polypeptide in tissue, as molecular weight markers and as a food CC supplement. (II) and its binding partners are useful in medical imaging CC supplement. (II) and its binding partners are useful for treating disorders involving aberrant protein expression or biological activity. The CC polypeptide and polynucleotide sequences have applications in CC polypeptide and polynucleotide sequences have applications in CC polypeptide and polynucleotide sequences have application of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this clattor, introduction format directly from MIPO at the printed specification, but was obtained in CC electronic format directly from MIPO at the printed specification of the sequence data for this content of the invention of the sequence content of the sequence content of the sequence data for this content of the sequence content of the sequence content of the sequence content of the sequence content of the sequence content of the sequence content of the sequence content of the sequence content of the sequence content of the sequence content of the sequence content of the sequence content of the sequence content of the sequence content of the sequence content of the sequence content of the seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
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23-AUG-2000; 2000US-00649167
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                                                                                         ACTGGGCCATCCGCGCCATCGAGACCCTCTCGGGTAAAGTGGAATTGCATGGGAAAATCA
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22-OCT-2001; 2001US-0341058P.
24-OCT-2001; 2001US-0343629P.
29-OCT-2001; 2001US-0349575P.
29-OCT-2001; 2001US-034957P.
25-UUN-2002; 2002US-0391342P.
01-OCT-2002; 2002US-00262445.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention describes an isolated polypeptide comprising any of 33 90 1273 amino acid sequences (I) given in the specification or its mature form, a sequence that is at least 95 % identical to (I), or a sequence comprising one or more conservative substitutions in the amino acid sequence of (I). The polypeptide is useful for preparing a composition for treating or preventing e.g. cancer. This sequence encodes a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New DAPK3 polypeptide, useful preventing e.g., cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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S, Millet I, Ooi
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WO200155322-A2

02-AUG-2001

31-UAN-2000; 04-FEB-2000; 24-FEB-2000; 02-MAR-2000; 16-MAR-2000; 17-MAR-2000; 18-APR-2000; 19-MAY-2000; 07-UUN-2000; 30-UUN-2000; 30-UUN-2000; 17-JAN-2001; 2000US-0180628P.
2000US-0184664P.
2000US-0189374P.
2000US-0199129P.
2000US-0199129P.
2000US-02015135P.
2000US-02014866P.
2000US-0211335P.
2000US-0211335P.
2000US-0211486P.
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2000US-0211487P.
2000US-0217487P.
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2000US-021748P.
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2000US-021748P.
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2000US-0221745P.
2000US-0225214P.
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2000US-0225268P.
2000US-0225757P.
2000US-022568P.
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2000US-0227182P.
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2000US-0227387P.
2000US-0227382P.
2000US-022882P. 2000US-0179065P 2001WO-US001341

2000US-0229343P. 2000US-0229344P. 2000US-0229345P. 2000US-0229509P.

2000US-0239513P. 2000US-0230437P. 2000US-0230438P.

01-SEP-2000; 01-SEP-2000; 01-SEP-2000; 05-SEP-2000; 06-SEP-2000; 06-SEP-2000; 06-SEP-2000; 06-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 14-SEP-2000; 14-SEP-2000;

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CC (ELISA). Disorders which are diagnosed or treated include autolimmune (CELISA). Disorders which are diagnosed or treated include autolimmune (CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. capplasms of the breast or liver, cardiovascular disorders e.g. carriest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, CC nervous system disorders e.g. Alzheimer's disease, infections caused by cateria, viruses and fungi and ocular disorders e.g. cormeal infection, CC and many other disorders listed in the specification. The polypeptides CC can also be used to aid wound healing and epithelial cell proliferation, CC transplantation, for supporting cell culture of primary tissues, to CC transplantation, for supporting cell culture of primary tissues, compabilities, fat content, lipid, protein, carbohydrate, vitamins, CC apabilities, fat content, lipid, protein, carbohydrate, vitamins, CC minerals, cofactors and other nutritional components. The present CC sequence encodes a novel secreted protein of the invention. Note: The content data for this patent did not form part of the printed
                                   δÃ
                                                                                Query Match
Best Local Similarity
Matches 1145; Conserv
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays enzyme linked immunosophant assays processes the protein and the protein can be used in the protein and the protein can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosophant assays are processed in the protein can be used in the protein can be used in the protein can be used in alleviating symptoms associated with the disorders and in diagnostic amunoassays e.g. radioimmunoassays or enzyme linked immunosophant assays are processed in the protein can be used in the pathological condition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid molecules encoding 461 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives.
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                                 CCCAGGCTGTGGGGGCCATCATCGGGAAGAAGGGGGGGCACACATCAAACAGCTGGCGAGAT 1306
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2000US-0249244P.
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2000US-0249265P.
2000US-0249265P.
2000US-0249299P.
2000US-024929P.
2000US-0250160P.
2000US-0250160P.
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2000US-0251989P.
2000US-0251990P.
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Pred. No. 6.8e-
3; Mismatches
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5.8e-281;
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2000US-0231242P 2000US-0231244P 2000US-0231244P 2000US-0231414P 2000US-0232881P 2000US-0232881P 2000US-0232398P 2000US-023239P 2000US-023239P 2000US-0232401P 2000US-0232401P 2000US-0232401P 2000US-0232401P 2000US-023401P 2000US-023401P 2000US-023401P 2000US-023401P 2000US-023401P 2000US-023401P 2000US-023401P 2000US-023401P 2000US-0236367P 2000US-0236367P 2000US-0236367P 2000US-0236370P 2000US-0237038P 2000US-0237039P 
29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
03-OCT-2000;
20-OCT-2000;
01-NOV-2000;
08-NOV-2000;

2000US-0241787P.
2000US-0241808P.
2000US-0241809P.
2000US-0244617P.
2000US-0246474P.
2000US-0246476P.
2000US-0246476P.
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2000US-0246525P.

2000US-0246526P.
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2000US-0249613P.
2000US-0249207P.
2000US-0249207P.
2000US-0249211P.
2000US-0249211P.
2000US-0249212P.

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GGGAAATCTCGTCGGAAGGACACT 2408		TAATTTTTTTTTTTTAAGAGAAAGCAGGCTTTTCTAGACTTTAAAGAATAAAGTCT 2324		ARTATETTTTAGAAATAATATATCAAATAACTCAACTTAACTCCAATTTTTAATCAATTAT 2264	TGTGGCCTGTGGGTTACACAGGGTGCCTGCAGCGGT	GCCAAGCAAAATGCACACCCTTTTTCTGTGGCAAATCGTCTCTGTACATGTGTGTACATA 2144	CCTSAACT CCCACGACGCTATCCCTTTTAGTTGAACTAACATAGGTGAACGTGTTCAAA 2084							AMALAMITOTICAGAATTATIGGGGGACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCA 443 GGGAAAATTG-TAAAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCA 1725 LULLILITTLICALICAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCA 1725	AAGTGATCGTCAGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCACACGCGAAGATCA 1666	AGAACTTAACCAGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGG 1606	ω	TGCCCTTTCCACAGCTGGCCGGGTGATTGGCAAAAGGTGGCAAGACCGTGAACGAAC	TCAGAG	TCATCATCACCGGGCCACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAAC 1426	TCGCCGGAGCCTCTATCAAGATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGG 1366
02-OCT-2000; 13-OCT-2000; 20-OCT-2000;	PR 02-OCT-2000; 2000US-0237037P. PR 02-OCT-2000; 2000US-0237038P. PR 02-OCT-2000; 2000US-0237039P.	29-SEP-2000 29-SEP-2000 02-OCT-2000	29-SEP-2000 29-SEP-2000 29-SEP-2000	PR 21-SEP-2000; 2000US-0234274P. PR 25-SEP-2000; 2000US-0234394P. PR 27-SEP-2000; 2000US-0235834P.	05-SEP-2000 08-SEP-2000 21-SEP-2000	01-SEP-2000 01-SEP-2000 05-SEP-2000	22-AUG-2000 30-AUG-2000 01-SEP-2000 01-SEP-2000	14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000	14-AUG-2000 14-AUG-2000 14-AUG-2000 14-AUG-2000	PR 11-JUL-2000; 2000US-0217496P. PR 14-JUL-2000; 2000US-0218290P. PR 26-JUL-2000; 2000US-0220963P. PR 26-JUL-2000; 2000US-0220964P.	28-JUN-2000 07-JUL-2000 07-JUL-2000 11-JUL-2000	17-JAN-2001; 31-JAN-2000; 04-FEB-2000;	19-SEP-2002.	OS Homo sapiens. XX PN US2002132753-A1.		gastrointestina hyperproliferat blood related d	Human; gene; ds; neural dis	DT 18-MAR-2003 (first entry) XX DE Human novel polynucleotide #739	ABX73911;	RESULT 12 ABX73911 ID ABX73911 standard; DNA; 1186 BP	Db 1163 GGGAAATCTCGTCGGAAGGACAC

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dard; DNA; 1186 first entry) ВP 1186

olynucleotide #739.

ds; neural disorder; immune system disorder; renal disorder; rder; respiratory disease; reproductive disorder; nal disorder; pulmonary disorder; cardiovascular disorder; ative disorder; inflammatory disease; allergic reaction; disorder; cancer; immunosuppressive; antiinflammatory; r; nephrotropic; cytostatic; antiallergic; thrombolytic; antiarteriosclerotic.

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(RUBE/)
(BARA/)
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               AAGTGATCGTCAGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCA
                                                                                     AGAACTTAACCAGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAATGAGG
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AAGTGATCGTCAGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCA
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RESULT 13
AAC66035
ID AAC66
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Best Local Similarity
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                                                                                                                                                                                                                                                                             The present invention describes human lung tumour proteins. Human lung tumour proteins and polynuclectides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, Teell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABI48959 to ABI49300 and ABB74946 to ABB75770 represent sequences used in the exemplification of the present
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Novel lung carcinoma polynucleotide sequences and polypeptides encoded the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer. γď

Claim 1; Page 337; 381pp; English.

The present invention describes isolated human lung carcinoma CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic comprising (I) or (II) can be used in gene therapy and in vaccines. Compositions CC comprising (I) or (II) can be used for stimulating an immune response in CC a patient and for treating lung cancer in a patient. Oligonucleotides of CI can be used for detecting the presence of a cancer in a patient, by CC obtaining a biological sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of polynucleotide that hybridises to the oligonucleotide and comparing the cCC amount of polynucleotide that hybridises to the oligonucleotide to a predetermined cut-off value, and determining the presence of a cancer in CC the patient. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. ABQ92145 to ABQ92486 and ABP61866 to invention

Sequence 1740 B₽; 526 A; 406 C; 417 G; 391 T; 0 U; 0 Other;

Matches Query Match

1116;

Conservative

Local

Similarity

21.2%;

Score 697.2; DB 6; Pred. No. 2.1e-174; 0; Mismatches 538;

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	1687 AAGCAGCAGGAGAATACCCTCAGGGAGTCGCCTCAC 1726 
1686 1680	1627 GGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCAGGGAAATTGTACAACAGGTG
1626 1620	1567 GTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTGATCGTCAGAATTATC
1566 1560	1507 CGGGTGATTGGCAAAGGTGGCAAGACCGTGAACGAACTGCAGAACTTAACCAGTGCAGAA
1506 1500	1447 AACCCCAAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCCACAGCTGGC
1446 1440	1387 GAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAACTGAAAGAGGAAAACTTCTTT
1386 1380	1327 ATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCATCACCGGGCCACCG
1326 1320	267 ATCGGGAAGAAGGGGGCACACATCAAACAGCTGGCGAGATTCGCCGGAGCCTCTATCAAG
1266 1260	209TTATCCAGAGCAGGAGATTGTGAATCTCTTCATCCCAACCCAGGCTGTGGGCGCCATC
1208 1200	163 GCCTGTACCCCCATCACCAGTTTGGCCCGGTTCCCGCATCATCACTC
1162 1140	GGATTAAATCTGAACGCCTTGGGTCTGTTCCCACCCACTTCA
1143 1080	AAATGATATGCTGGCTGTTAACACC           AAAATGATATTGCTTCTATGAATCTT
1083	1024 TACAACCCGGAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCCTGTGCCAGTGCTGAG
1023 960	964 AAAATTGAACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCATA:
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903 940	844 CTTGAAATCATGCAGAAAGAGGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTGAAA 9
343 780	784 GAGAAGCCTGTCACCATCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGCATGATT 8
783 720	724 ATCACTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAACTCTGGAGCTGCA 7

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(GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tseng
APPLICANT: Gure, Ali
APPLICANT: Stockert, Elisabeth
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APPLICANT: Muth, Alexander
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APPLICANT: Old, Lloyd J

TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Canc
TITLE OF INVENTION: Associated
TITLE OF INVENTION UNMER: US/09/899,651
CURRENT APPLICATION NUMBER: US/09/899,651
PRIOR APPLICATION NUMBER: US/09/861,709
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; SEQ ID NO 8
; LENGTH: 3283
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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60	272 TTTTCTTTTAAAGAGAAAGCAGGCTTTTCTAGACTTTAAAGAATAAAGTCTTTGG	
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31	AGCCATCCACTTCACCATCCACTCGGATCTCTCCTGAA 20 	
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11 40	352 GAATGAGAAGTCTGCGGAGGGCGGCCAGGGACTCTGCCGAGGGCCCTGAGAACCCCCAGGGGC 19 	
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RESULT 4

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; Sequence 6, Application US/09899651

; Patent No. 6576756

; GENERAL INFORMATION:
APPLICANT: Gure, Ali
APPLICANT: Tsang, Solam
APPLICANT: Stockert, Elisabeth
APPLICANT: Jager, Elke
APPLICANT: Muth, Alexander
APPLICANT: Old, Lloyd J.

; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer
ITITLE OF INVENTION: Associated
; TITLE OF INVENTION: Associated
; TITLE OF INVENTION IMBER: US/09/899,651
; CURRENT APPLICATION NUMBER: US/09/899,651
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/861,709

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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: MCNeill, Patricia D.
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 347
LENGTH: 1740
TYPE: DNA
ORGANISM: Homo sapiens
US-09-643-597-347
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US-09-643-597-347
; Sequence 347, Application
; Patent No. 6426072
; GENERAL INFORMATION:
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                                               GTGGAATTGCATGGGAAATCATGGAAGTTGATTACTCAGTCTCTAAAAAAGCTAAGGAGC
                                                                                       TTCGTGGACTGCCCGGACGAGAGCTGGGCCCTCAAGGCCATCGAGGCGCTTTCAGGTAAA
                                                                                                           TTCGTGGACTACCCCGAGCCAGAACTGGGCCATCCGCGCCATCGAGACCCTCTCGGGTAAA
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Li, Samuel X.
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Hosken, Nancy
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; LENGTH: 11740
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-542-615A-347
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APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: FADGER, GATY R.
APPLICANT: Hosken, Nancy A.
APPLICANT: COMPOUNDS AND METHODS FO TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-542-615A-347
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APPLICANT: Wang, To
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APPLICANT: Kalos, M
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APPLICANT: Bangur,
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Best Local Similarity 64.9%;
Matches 1116; Conservative
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APPLICANT: KAIDS, Michael D.
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APPLICANT: Fanger, Gary R.
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COMPOSITIONS AND METHODS FOR THE THERAPY
FILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT APPLICATION NUMBER: US/09/606,421B
NUMBER OF SEQ ID NOS: 358
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SOFTMARE: FASTSER FOR Windows Version 3.0
SEQ ID NO 347
LENGTH: 1740
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APPLICANT: Chen, Yao-Tseng
APPLICANT: Chen, Yao-Tseng
APPLICANT: Gure, Ali
APPLICANT: Tsang, Solam
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Old, Lloyd J
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
ITILE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
CURRENT APPLICATION NUMBER: US/09/061,709B
CURRENT FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
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Best Local Similarity 64.8%;
Matches 1115; Conservative
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                                                                  TTCGTGGACTGCCCGGACGAGAGCTGGGCCCTCAAGGCCATCGAGGCGCTTTCAGGTAAA
                                                                                                                                           ATCTTCAAGGACGCCAAGATCCCGGGTGTCGGGACCCTTCCTGGTGAAGACTGGCTACGCG
                                                                                                                                                                        CTCTTTGGGGACAGGAAGCTGCCCCTGGCGGACAGGTCCTGCTGAAGTCCGGCTACGCC 192
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Pred. No. 2.5e-184;
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ATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCATCACCGGGCCACCG 1386
                                    ATCGGCAAGCAGGCCAGCACATCAAGCAGCTTTCTCGCTTTGCTGGAGCTTCAATTAAG
                                                                                                                                             --TTATCCAGAGCAGGAGATTGTGAATCTCTTCATCCCAACCCAGGCTGTGGGCGCCATC
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                                                                         ATCGGGAAGAAGGGGGGACATCAAACAGCTGGCGAGATTCGCCGGAGCCTCTATCAAG
                                                                                                                   GAGCAATCAGAAACGGAGACTGTTCATCAGTTATCCCAGCTCTATCAGTCGGTGCCATC
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APPLICANT: Jager, Elke
APPLICANT: Knuth, Alexander
APPLICANT: Old, Lloyd J.

TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer
TITLE OF INVENTION: Associated
TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
FILE REFERENCE: LUD 538
CURRENT APPLICATION NUMBER: US/09/899,651
CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US/09/061,709
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 4
LENGTH: 4159
TYPE: DNA
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Best Local Sim
Matches 1115;
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Patent No. 6576756
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APPLICANT: Gure, Ali
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:

APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Hosken, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
APPLICANT: Hanger, Gary R.
APPLICANT: Hanger, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Henderson, Robert A.
APPLICANT: Menderson, Robert A.
APPLICANT: MORE COMPOSITIONS AND METHOD
ITITLE OF INVENTION: AND DIAGNOSIS OF LUNG C
FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
                                                                                                                                                                                                                                                            LENGTH: 4181
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
; NAME/KEY: unsure
; NAME/KEY: unsure
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OTHER INFORMATION: n
NAME/KEY: unsure
LOCATION: (3502)
OTHER INFORMATION: I
NAME/KEY: unsure
LOCATION: (3506)
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                                                             LOCATION: (3506)
OTHER INFORMATION: 1
NAME/KEY: unsure
LOCATION: (3520)
OTHER INFORMATION:
NAME/KEY: unsure
LOCATION: (3538)
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Query Match  Query Matchas Similarity 64.8%; Pred. No. 2.6e-184;  Best Local Similarity 64.8%; Pred. No. 2.6e-184;  Matches 1115; Conservative 07, Mismatches 539; Indels 66; Gaps 3,  Matches 1115; Conservative 07, Mismatches 539; Indels 66; Gaps 3,  Property Matchas 115; Conservative 07, Mismatches 539; Indels 66; Gaps 3,  Matches 1115; Conservative 07, Mismatches 539; Indels 66; Gaps 3,  Property Match 115; Conservative 07, Mismatches 539; Indels 66; Gaps 3,  Matches 1115; Conservative 07, Mismatches 539; Indels 66; Gaps 3,  Property Match 115; Conservative 07, Mismatches 539; Indels 66; Gaps 3,  Matches 1115; Conservative 07, Mismatches 539; Indels 66; Gaps 3,  Matches 1115; Conservative 07, Mismatches 539; Indels 66; Gaps 3,  Property Matches 112,  Matches 112,  Matches 112,  Matches 112,  Mismatches 539; Indels 66; Gaps 3,  Mismatches 539; Indels 66; Gaps 66; Gaps 3,  Mismatches 539; Indels 66; Gaps 66; Gaps 66; Gaps 66; Gaps 67;	OTHER INFORMATION: n=A,T,C or G NAME/KEY: unsure LOCATION: (3549) OTHER INFORMATION: n=A,T,C or G NAME/KEY: unsure LOCATION: (3646) OTHER INFORMATION: n=A,T,C or G NAME/KEY: unsure LOCATION: (3940) OTHER INFORMATION: n=A,T,C or G NAME/KEY: unsure LOCATION: (3968) OTHER INFORMATION: n=A,T,C or G NAME/KEY: unsure LOCATION: (3968) OTHER INFORMATION: n=A,T,C or G NAME/KEY: unsure LOCATION: (4036) OTHER INFORMATION: n=A,T,C or G NAME/KEY: unsure LOCATION: (4062) OTHER INFORMATION: n=A,T,C or G NAME/KEY: unsure LOCATION: (4068) OTHER INFORMATION: n=A,T,C or G NAME/KEY: unsure LOCATION: (4068) OTHER INFORMATION: n=A,T,C or G NAME/KEY: unsure LOCATION: (4068) OTHER INFORMATION: n=A,T,C or G NAME/KEY: unsure LOCATION: (4068) OTHER INFORMATION: n=A,T,C or G NAME/KEY: unsure LOCATION: (4068) OTHER INFORMATION: n=A,T,C or G NAME/KEY: unsure LOCATION: (4016) OTHER INFORMATION: n=A,T,C or G NAME/KEY: unsure LOCATION: (4016) OTHER INFORMATION: n=A,T,C or G NAME/KEY: unsure LOCATION: (4016) OTHER INFORMATION: n=A,T,C or G NAME/KEY: unsure NAME
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; LOCATION: (1)...(4181)
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US-09-480-884A-175
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APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Hosken, Nancy A.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CA.
FILE REFERENCE: 210121.455C6
CURRENT APPLICATION NUMBER: US/09/480,884A
CURRENT FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 330
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LENGTH: 4181
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TITLE OF INVENTION: AND DIAGNOSIS
TITLE OF ENERGINE: 210121.4556
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CURRENT FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
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Kalos, Michael D.
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Sequence 175, Application US/09606421B
Patent No. 6531315
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy
                                                                                                                                                                              RESULT 13
US-09-606-421B-175
   APPLICANT:
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Fanger, Gary R.
Li, Samuel X.
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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION UMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 175
                                                                                                                                   FEATURE:
NAME/KEY: unsure
LOCATION: (4056)
OTHER INFORMATION:
                                                                                                                                                                                          FEATURE:
NAME/KEY: unsure
(4036)
                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: unsure
LOCATION: (3968)
OTHER INFORMATION: 1
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NAME/KBY: unsure
LOCATION: (3940)
OTHER INFORMATION: )
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NAME/KEY: (3502)
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NAME/KEY: unsure
LOCATION: (3347)
OTHER INFORMATION: 1
         NAME/KEY: unsure
LOCATION: (4088)
                                  LOCATION: (4080)
OTHER INFORMATION:
FEATURE:
                                                                  NAME/KEY:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: (3538)
OTHER INFORMATION:
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LOCATION: (3506)
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LOCATION: (3646)
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TYPE: DNA
ORGANISM: Homo sapiens
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; ORGANISM: Mus musculus US-09-261-855-1

LENGTH: 22 TYPE: DNA

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REGION DETERMINANT-BINDING NUCLEIC ACID SEQUENCE

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APPLICANT: Gure, Ali
APPLICANT: Stockert, Elisabeth
APPLICANT: Stockert, Elisabeth
APPLICANT: Muth, Alexander
APPLICANT: Muth, Alexander
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer As
TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
FILE REFERENCE: LUD 5538
CURRENT APPLICATION NUMBER: US/09/061,709B
CURRENT FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
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GENERAL INFORMATION:
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1683 GGTGAAGCAGCAGGAGAAATACCCTCAGGGAGTCGCCTCACAGCGCAGCAGCTAAGG 1742	Qy Db
	Qy Db
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1503 TGGCCGGGTGATTGGCAAAGGTGGCAAGACCGTGAACGAAC	g 80
1443 CTTTAACCCCAAAGAAGTGAAGCTGGAAGCGCATAICAGAGTGCCCTCTTCCACAGC 1502	Qy db
1383 ACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAACTGAAAGAGGAAACTT 1442 	gg Qy
1323 CAAGATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCACCGGGCC 1382	g &
1263 CATCATCGGGAAGAAGGGGGCACATCAAACAGCTGGCGAGATTCGCCGGAGCCTCTAT 1322	Db Qy
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Search completed: July 24, 2004, 16:48:44 Job time : 248.862 secs

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Result
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Copyright (c) 1993 - 2004 Compugen Ltd
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9 US-09-764-864-329

9 US-09-764-864-332

16 US-10-262-445-39

9 US-09-764-864-749

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Sequence 8, Appli
Sequence 20241, Ap
Sequence 146, Appl
Sequence 48, Appl
Sequence 329, App
Sequence 329, App
Sequence 339, Appl
Sequence 39, Appl
Sequence 749, App
Sequence 347, App
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	-10-313-986-42	-10-117-982-4	700-42	-897-778-428	09-850-716A-42	US-10-116-802-145	US-10-313-986-175	US-10-117-982-175	US-10-007-700-175	US-09-466-396A-175	09-897-778-175	US-09-850-716A-175	-954	05-	-899-65	0-313-986-4	-10-117-982-48	-10-313-986-47	-10-117-982-4	0-313-986-48	3-986-45	0-313-986-4	-10-117-982-45	-10-117-982-4	-10-007-70	S-10-007-700-4	7-778-	09-897-778-447	-10-313-986-4	-10-313-986-	82-4
1	4	equence 428	e 428		quence 428,	145	Sequence 175, App	175	e 175	e 175	Sequence 175. App	e 175.	equence 71	<u> </u>	4	.r.	Φ.	Sequence 479, App	æ			447.	Sequence 450. App	447	መ '	e 447	450.	quence 447,	e 478	equence 347.	Sequence 478, App

## ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/09/899,651
CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US/09/061,709
PRIOR ETILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 8
LENGTH: 3283
TYPE: DNA
ORGANISM: Homo sapiens
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Patent No. US20020111470A1
                                                                                                                    Matches 3283;
                                                                                                                                       Query Match
Best Local 9
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APPLICANT: Jager, Elke
APPLICANT: Jager, Elke
APPLICANT: Odd, Lloyd J.

ITILE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer
TITLE OF INVENTION: Associated
TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
FILE REFERENCE: LUD 5538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                     FEATURE:
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61 AAGAGACGGATGATGAACAAGCTTTACATCGGGAACCTGAGCCCCGCCGTCACCGCCGAC
                                                          1 GGCAGCGGAGGAGCGAGGAGCGCCGGGTACCGGGGCCGGGGGAGCCGCGGGGCTCTCGGGG
                                                                                                            h 100.0%; Score 3282; Similarity 100.0%; Pred. No. 0; 83; Conservative 0; Mismatches
                                      Tsang, Solam
Stockert, El:
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121 GACCITCGGCARCCTCTTTGGGGAAACCTGACCGGGAACCTGACCCGGGGAACCTGACCCGGGAACCTGACCGGCAACCTGACGGCAACCTGACGGCAACCTGACGGCAACCTGACGGCAACCTGACGCGGGAACCTGACGCGGAACCTGACGCGAACCCGACGGGGAACCCGACGGGGAACCCGACGGGGAACCCGACGGGGAACCCGACGGGGAACCCGACGGGGAACCCGACGGGGAACCCGACGGAACCCGACGGGGAACCCGACGGGGAACCCGACGGGGAACCCGACGGGGAACCCGACGGGGAACCCGACGGGGAACCCGACGGGGAACCCGACGGGGAACCCGACGGGGAACCCGACGGGGAACCCGACGCGACGGGGAACCCGACGGGGAACCCGACGGGGAACCCGACGGGGAACCCGACGGGGAACCCGACGGGGAACCCGACGGGGAACCCGACGGGGAACCGACGGGGAACCGACGGGGAACCGACGGGGAACCCACGGGGAACCGACGGGGAACCGACGGGGAACCGACGGGGAACCGACGGGGAACCGACGGGGAACCGACGGGGAACCGACGGGGAACCGACGGGGAACCGACGGGGAACCGACGGGGAACCGACGGGGAACCGACGGGGAACCGACGGGGAACCGACGGGGAACCGACGGGGAACCGACGGGGAACCGACGGGGAACCGACGGGGAACCACGGGGAACCACGGGGAACCACGGGGAACCACGGGGAACCACGGGAACCAACGGCAACACGGAACCAACCGACGGGAACAAC
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1141 ACCACTCOGGATACTTCTCCCAGCCTGTACCCCATCACCAGTTTGGCCCCGTTCCCGGAT 1200 1201 CARCACTCTTATCCAGAGCAGAGAATTGTGAATCTCTTCATCCCAGACCTAGCCAGAGCTTGGCCCAGCCTGTTGGCCCAGCCCAGCCTGTTGGCCCAGCCCAGCCTGTTGGCCCAGCCCAGCCTGTTGGCCCAGCCCAGCCTGTTGGCCAACCCAGAGCCCAGAACCAAACCCCAGAACCCAGAACCCAGAACCCAGAACCCAGAACCCAGAACCCAGAACCCAGAACCCAGAACCCAGAACCCAGAACCCAGAACCCAGAACCCAGAACCCAGAACCCAGAACCCAGAACCAGAACCAAACCCAGAACCAGAACCCAGAACCCAGAACCAACCACC

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RAPPLICANT: LAC, John
APPLICANT: Lee, John
APPLICANT: Lillie, James
FILLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
FILE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
FILE REFERENCE: MRI-006B
CURRENT APPLICATION INDENTIFICATION, ASSESSMENT, PREVENTION, AND
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: US 60/207,124
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR RILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/216,820
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR APPLICATION NUMBER: US 60/220,661
PRIOR APPLICATION NUMBER: US 60/257,672
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PRIOR APP
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; LOCATION: 1, 3897, 3898, 3899, 3900, 3901, 3902, 3903, 3904, 3905
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-20241
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                       AGAAACCGCCGTTGTCAACGTCACATATGCAACAAGAGAAGAAGAAGCAAAAATAGCCATGGA
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Pred. No. 0;
0; Mismatches
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APPLICANT: Xunei ZHAO

APPLICANT: Karen GLATT

ITILE OF INVENTION: Nucleic Acid Molecules and Proteins For The TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ova: CURRENT APPLICATION NUMBER: US/10/097,340

CURRENT FILING DATE: 2002-03-14

PRIOR APPLICATION NUMBER: 60/276,025

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/325,149

PRIOR FILING DATE: 2001-03-6

PRIOR APPLICATION NUMBER: 60/276,026

PRIOR APPLICATION NUMBER: 60/276,026

PRIOR APPLICATION NUMBER: 60/276,026

PRIOR FILING DATE: 2001-03-14
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APPLICANT: Manjula GANNA
APPLICANT: Sebastian HOEI
APPLICANT: Shubhangi KAM
APPLICANT: Steve G. KOVA:
APPLICANT: Rachel E. MEYYI
APPLICANT: Michael MORRIS
APPLICANT: Michael MORRIS
APPLICANT: Michael MORRIS
APPLICANT: Peter OLANDT
APPLICANT: Ami SEN
APPLICANT: Peter VEIBY
APPLICANT: Robert C. BAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 146, Application US/10097340 Publication No. US20030087250A1 GENERAL INFORMATION:
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PRIOR FILING DATE: 2001/09/26
PRIOR PPLICATION NUMBER: 60/311,732
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
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QY 363 GGATGGACTTTTGGCTCAATATGGGACAGTGGAGAATGTGGAACAAGTCAACACAGACAC 422	Qy 303 GCTAAGGAGCAGGAAAATTCAGATTCCGAAACATCCCTCCTCACCTGCAGTGGGAGGTGTT 362	Qy 243 CTCGGGTAAAGTGGAATTGCATGGAAAATCATGGAAGTTGATTACTCAGTCTCTAAAAA 302	QY 183 CGGCTACGCCTTCGTGGACTACCCCGACCAGAACTGGGCCATCGGCGCCATCGAGACCCT 242	Qy 123 CCTCCGGCAGCTCTTTGGGGACAGGAAGCTGCCCCTGGCGGGACAGGTCCTGCTGAAGTC 182	QY 63 GAGACGGATGAACAAGCTTTACATCGGGAACCTGAGCCCCGCCGTCACCGCCGACGA 122	S = S	Query Match 99.1%; Score 3253.8; DB 17; Length 3667; Best Local Similarity 99.8%; Pred. No. 0; Matches 3277; Conservative 0; Mismatches 3; Indels 2; Gaps 2;	; LENGIH: 3667 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-648-593-48	ro.		APPLICANT: Bristol-Myers Squibb Company  TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT  TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR  TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS	0 = 0	RESULT 4	3242				3062	a
Qy	Οy	Db Vy	Qу	QQ da	g dg	D Q	Qy Db	ДУ	dd Qy	Qy Db	QY dd	Qy Db	Qγ	D QQ	ДĎ	& B	, VQ	9d V2	DЪ
1443 CTTTAACCCCAAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCCACAGC 1502	1383 ACCGGAAGCCCAGTTCAAGGCCCACGGACGGACTCTTTGGGAAACTGAAAGAGGAAAACTT 1442 	1323 CAAGATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCATCACCGGGCC 1382 		1203 TCACTCTTATCCAGAGCAGGAGATTGTGAATCTCTTCATCCCAACCCAGGCTGTGGGCGC 1262	1143 CCACTCCGGATACTTCTCCAGCCTGTACCCCCATCACCAGTTTGGCCCGTTCCCGCATCA 1202	1083 GATAGAGATTATGAAGAAGCTGCGTGAGGCCTTTGAAAATGATATGCTGGCTG	1023 ATACAACCCGGAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCCTGTGCCAGTGCTGA 1082 	963 GAAAATTGAACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCAT 1022 	903 AATCTTGGCACACAATGGCTTGGTTGGAAGACTGATTGGAAAAGAAGGCAGAAATTTGAA 962 	843 TCTTGAAATCATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTGAA 902 	783 AGAGAAGCCTGTCACCATCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGCATGAT 842	723 CATCACTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAACTCTGGAGCTGC 782 	663 CCTGGTCCCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAGAA 722	603 GCAAGGCCACGCCCCTGGGGGGACACTTCTCAGGCCAGACAGA		849 GAAGCTAAGCGGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCCGGGATGA 908 543 AGAGGTGAGCTCCCCTTCGCCCCCTCAGCGAGCCCAGCGTGGGGACCACTCTTCCCCGGGA 602	483 GAAGCTAAGCGGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCCTACATCCCGGGATGA 542	423 AGAAACCGCCGTTGTCAACGTCACATATGCAACAAGAAGAAGAAGCAAAAATAGCCATGGA 482 	

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	2523 CACAGGITITAAACIGGITITITGCATACIGCTATATAATTCTCTGTGTCTCTCTCTCTTTTA 2582
., ., .,	2463 AAGAAGAAACTCTGTCACTCCTCATGCCTGTCTAGCTCATACACCCCATTTCTCTTTGCTT 2522
×, ×, ×, ×,	2403 GACACTCACGGCAGTTCTGGATCACCTGTGTATGTCAACAGAAGGGATACCGTCTCCTTG 2462
	2343 TAGAGAGGAGCTTTGAGGCCACCCGCACAAAATTCACCCAGAGGGAAATCTCGTCGGAAG 2402 
a o	2283 AAAGAGAAAGCAGGCTTTTCTAGACTTTAAAGAATAAAGTCTTTTGGGAGGTCTCACGGTG 2342 
RES; S; P	2223 TATATCAAATAACTCAACTAACTCCAATTTTTAATCAATTATT
מם	2163 AAGATATGTGGCCTGTGGGTTACACAGGGTGCCTGCAGCGGTAATATATTTTTAGAAATAA 2222 
Qy Oy	2103 CCTTTTTCTGTGGCAAATCGTCTCTGTACATGTGTACATATTAGAAAGGGAAGATGTT 2162 
Db Qy	2043 CTATCCCTTTTAGTTGAACTAACATAGGTGAACGTGTTCAAAGCCAAGCAAAATGCACAC 2102 
Qv Qv	1983 CTGCAGGCTTCAGCCATCCACTTCACCATCCACTCGGATCTCTCCTGAACTCCCACGACG 2042
QV QQ	1923 GGGGAAGGTCAGCCAGGTTTGCCAGAACCACCGAGGCCCCGCCTCCCGCCCCCAGGGCTT 1982
νο dα	1863 CTGCGGAGGCGGCCAGGGACTCTGCCGAGGGCCCTGAGAACCCCCAGGGGCCGAGGAGGAGGGGC 1922
ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο	1803 AGACCAAACGCAGCCAGCCAGATCGGGAGCAAACCAAAGACCATCTGAGGAATGAGAAGT 1862 
, מם מם	1743 CTCCCACAGGCACCAGCAAAACAACGGATGAATGTAGCCCTTCCAACACCTGACAGAATG 1802 
QQ dd	1683 GGTGAAGCAGCAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGCAGCAAGTGAGG 1742 
ο dg .	1623 TATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCAGGGAAATTGTACAACA 1682 
OV OV	1563 AGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGGAAGTGATCGTCAGAAT 1622 
OV DD 12	1503 TGGCCGGGTGATTGGCAAAGGTGGCAAGACCGTGAACGAAC
	1809 CTTTAACCCCAAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCCACAGC 1868

US-09-899-651-6
; Sequence 6, Application US/09899651
; Patent No. US20020111470A1
; Patent No. US20020111470A1
; Patent No. US20020111470A1
; GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tseng
APPLICANT: Gure, Ali
APPLICANT: Tsang, Solam
; APPLICANT: Knuth, Alexander
APPLICANT: Knuth, Alexander
APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer
ITILE OF INVENTION: Associated
ITITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
; FILE REFERENCE: LUD 5538
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/899,651
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/899,651
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 6
; LENGTH: 3412

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901 AAAATCTTGGCACACAATGGCTTGGTTGGAAAACTGATTGGAAAAGAAGGCAGAAATTTG 96	DD 841 ATTCTTGAAATCATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTG 900  901 AAAATCTTGGCACAAATGGCTTGGTTGGAAAGATTGGAAAAAGAAGGAAG	841 ATTCTTGAAATCATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTG 9	OY 781 GCAGAGAAGCCTGTCACCATCCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGCATG 840	Oy 721 AACATCACTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAACTCTGGAGCT 780	Qy 661 ATCCTGGTCCCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAG 720	Qy 601 GAGCAAGGCCACGCCCTGGGGGCACTTCTCAGGCCAGACAGA	QY 541 GAAGAGGTGAGCTCCCCTTCGCCCCCTCAGCGAGCCCAGCGTGGGGACCACTCTTCCCGG 600 [	QY 481 GAGAAGCTAAGGCGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCCGGAT 540	Qy 421 ACAGANACCGCCGTTGTCAACGTCACATATGCNACAAGAGAAGAAGAAAATAGCCATG 480	Qy 361 TTGGATGGACTTTTGGCTCAATATGGGACAGTGGAGAATGTGGAACAAGTCAACAGAC 420	Qy 301 AAGCTAAGGAGGAGGAAAATTCAGATTCGAAACATCCCTCCTCACCTGCAGTGGGAGGTG 360	QY 241 CTCTCGGGTAAAGTGGAATTGCATGGGAAAATCATGGAAGTTGATTACTCAGTCTCTAAA 300	Qy 181 TCCGGCTACGCCTTCGTGGACTACCCCGACCAGAACTGGGCCATCCGGGCCATCGAGACC 240	Qy 121 GACCICCGGCAGCICTITGGGGACAGGAAGCIGCCCCIGGCGGGACAGGICCTGCAGG 180 [	Qy       61 AAGAGACGGATGATGAACAAGCTTTACATCGGGAACCTGAGCCCGGCCGTCACCGCCGAC       120	Qy 1 GGCAGCGGAGGAGGAGGAGGAGGAGCCGGGGTACCGGGGCGGGGGAGAGCCGCGGGGCTCTCGGGG 60	Query Match 95.7%; Score 3143; DB 9; Length 3412; Best Local Similarity 96.2%; Pred. No. 0; Matches 3283; Conservative 0; Mismatches 0; Indels 129; Gaps 1;	; TYPE: DNA ; ORGANISM: Homo sapiens ; PEATURE: US-09-899-651-6
Qy B	Q	Qy dd	Db Oy	Ωy	Db Qy	рь	db Qy	Db Qy	Qγ	Db Qq	Db Qy	Db Qy	dg VQ	DB 45	}	QQ dg	QY Db	Qy Db
1981 GAATGAGAAGTCTGCGGAAGGCCAGGGACTCTGCCGAGGCCCTGAGAACCCCAGGGGC 2040 1912 CGAGGAGGGGCGGGGAAAGGTCAGCCAGGTTTGCCAGAAACCACCGAGCCCCCCCC	852 GAATGAGAAGTCTGCGGAGGCGGCCAGGGACTCTGCCGAGGCCCTGAGAACCCCCAGGGC	1792 CTGACAGAATGAGACCAAACGCAGCCAGATCGGGAGCAAACCAAAGACCATCTGAG 1851 	1732 AGCAACTGAGGCTCCCACAGGCACCAGCAAACCAACGGATGAATGTAGCCCTTCCAACAC 1791	672 ATTGTACAACAGGTGAAGCAGCAGGAGCAGAATACCCTCAGGGAGTCGCCTCACAGGG	612 ATCGTCAGAATTATCGGGCACTTCTTTGCTAGCCACACTGCACAGCGCAAGATCAGGGAA	552 681	1492 TCTTCCACAGCTGGCCGGGTGATTGGCAAAAGGTGGCAAGACCGTGAACGAAC	1432 GAGGAAACTTCTTTAACCCCAAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCC 1491 	1372 ATCACCGGGCCACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAACTGAAA 1431 	1312 GAGCCTCTATCAAGATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATC 1371	1252 GCTGTGGGCGCCATCATCGGGAAGAAGGGGGCACACATCAAACAGCTGGCGAGATTCGCC 1311	1192 TTCCCGCATCATCACTCTTATCCAGAGCAGGAGATTGTGAATCTCTTCATCCCAACCCAG 1251	1141ACCCACTCCGGATACTTCTCCAGCCTGTACCCCCATCACCAGTTTGGCCCG 1191 1261 CCCTTCACTACCCACTCCGGATACTTCTCCAGCCTGTACCCCCATCACCAGGTTTGGCCCG 1320	1201 CTGTCCGTGCTATCTCCACCAGCAGGGGCCCCGCGGAGCTCCCCCCGCTGCCCCCTACCAC 1260	CAACAAGCCAATCTGATCCCAGGGTTGAACCTCAGCGCACTTGGCATCTTTTCAACAGGA	GAGATAGAGATTATGAAGAAGCTGCGTGAGGCCTTTGAAAATGATATGCTGGCTG	1021 ATATACAACCCGGAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCCTGTGCCAGTGCT 1080	

992 CAGGGCGTTAAATTCACAGATTTTTTTTAACGAGAAAAACACACAGAAGAGCTZ
2932 ATTCCTTTCTTTAAAAAAAAAATGTGGAGGAAAGTAGAAATTTACCAAGGTTGTTGGCC 2991 
872 AAAGAATGTATTTTGTCI
2812 AGGAAAACAGGAACCCACCAAACCAACCAATCAACCAAAGAAAAAATTCCACAATG 2871 
2752 CTTACACTTGGTTACTCAAAAGAACAAGAGTCAATGGTACTTGTCCTAGCGTTTTTGGAAG 2811
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2632 TTTCCTCATCCCTCCATCTCAATCCCGTATCTACGCACCCCCCCC
2572 CTCTCTGTTTATCTCTCCCCTCCCTCCCCTCCCCTTCTCTCCCATCTCCATTCTTTGAA 2631
2512 TCTCTTTGCTTCACAGGTTTTAAACTGGTTTTTTGCATACTGCTATATAATTCTCTGTCT 2571
2452 CCGTCTCCTTGAAGAGGAAACTCTGTCACTCCTCATGCCTGTCTAGCTCATACACCCATT 2511
2392 CTCGTCGGAAGGACACTCACGGCAGTTCTGGATCACCTGTGTATGTCAACAGAAGGGATA 2451
2332 GTCTCACGGTGTAGAGAGGAGCTTTGAGGCCACCCGCACAAAATTCACCCAGAGGGAAAT 2391
2272 TTTTCTTTTAAAGAGAAAAGCATTTCTAGACTTTAAAGAATAAAGTCTTTGGGAG 2331 
2212 TTTAGAAATAATATATCAAATAACTCAACTAACTCCAATTTTTAATCAATTATT
2152 GGGAAGATGTTAAGATATGTGGCCTGTGGGTTACACAGGGTGCCTGCAGCGGTAATATAT 2211
2092 AAAATGCACACCCTTTTTCTGTGGGCAAATCGTCTCTGTACATGTGTGTACATATTAGAAA 2151 
2032 CTCCCACGACGCTATCCCTTTTAGTTGAACTAACATAGGTGAACGTGTTCAAAGCCAAGC 2091
1972 CCCCAGGGCTTCTGCAGGCTTCAGCCATCCACTTCACCATCCACTCGGATCTCTCCTGAA 2031

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Qy 488 TAAGCGGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACA,TCCCGGATGAAGAGG	OY 428 CCGCCGTTGTCAACGTCACATATGCAACAAGAGAAGAAGAAAATAGCCATGGAGAAAGC 	Qy 368 GACTTTTGGCTCAATATGGGACAGTGGAGAATGTGGAACAAGTCAACACACAGACACAGACACAGAAAA	Qy 308 GGAGCAGGAAAATTCAGATTCGAAACATCCCTCCTCACCTGCAGTGGGAGGTGTTGGATG	Qy 248 GTAAAGTGGAATTGCATGGGAAATCATGGAAGTTGATTACTCAGTCTCTAAAAAGCTAA	Qy 188 ACGCCTTCGTGGACTACCCCGACCAGAACTGGGCCATCCGCGCCATCGAGACCTCTCGG	Qy 128 GGCAGCTCTTTGGGGACAGGAAGCTGCCCCTGGCGGACAGGTCCTGCTGAAGTCCGGCT	QY 68 GGATGATGAACAAGCTTTACATCGGGAACCTGAGCCCGCCGTCACCGCCGACGACCTCC	Query Match 93.0%; Score 3052.6; DB 9; Length 369 Best Local Similarity 96.0%; Pred. No. 0; Matches 3214; Conservative 1; Mismatches 1; Indels 132	Qy  3052 GTGTTTTACCTCAGGACCTTGGTGTGTTTGTTTTGTAAAAATTAGATTAGATAAAATTACCTGATAG Qy 3181 GTGTTTTACCTCAGCACCTTGGTGTTTTGTTTTGTAAAAAAAA
CGGATGAAGAGG 547	4u nu	'AGACACAGAAA 427             AGACACAGAAA 450					CGACGACCTCC 127		AAAGCTGATAG 3111

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1379 GGCCACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAACTGAAAGAGGAAA 1438	1259 GCGCCATCATCGGGAAGAAGGGGGCACACATCAAACAGCTGGCGAAGATTCGGCCGGAGCCT 1318	1141 ACCCACTCCGGATACTTCTCCAGCCTGTACCCCCATCACCAGTTTGGCCCGTTCCCGC 1198	CCAATCTGAT	11	TTGAACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCATATACA 	848 AAATCATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTGAAAAATCT 907	751 CTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAAAAA	68 TC	548 TGAGCTCCCCTTCGCCCCTCAGCGAGCCCAGCGTGGGGACCACTCTTCCCGGGAGCAAG 607	
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2459 CITGAAGAGGAAACTCTGTCACTCCCATGCCTGTCTAGCTCATACACCCATTTCTCTTT	GAA		251 159 311	2131 GETTETGGGGGETTCAGCCATCCACTTCACCATCCACTCGGATCTCTCCTGAACTCCCAC 2039 GACGCTATCCCTTTTAGTTGAACTAACATAGGTGAACGTGTTCAAAGCCAAGCAAAATGC	1919 GGGCGGGAAGGTCAGCCAGGTTTGCCAGAACCACCGAGCCCCGCCTCCCGCCCCCCAGG	51 59 59	31 39 91	9 GAATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGCGCAAGATCAGGG	1499 CAGCTGGCCGGGTGATTGGCAAAGGTGGCAAGACCGTGAACGAAC	

RESULT 7  US-09-764-864-332 ; Sequence 332, Application US/09764864 ; Patent No. US20020132753A1 ; GENERAL INFORMATION:     Applicant Patent No. US20020132753A1 ; GENERAL INFORMATION: Nucleic Acids, Proteins, and Antibodies     TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies     FILE REFERENCE: PTZ23     CURRENT FILLING DATE: 2001-01-17     Prior application data removed - consult PALM or file wrapper     NUMBER OF SEQ ID NOS: 1792     SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 332 ; SOFTWARE: PATENTIAL PALM OR FILE Wrapper     NUMBER OF SEQ ID NOS: 1792 ; SOFTWARE: PATENTIAL PALM OR FILE Wrapper     NUMBER OF SEQ ID NOS: 1792 ; SOFTWARE: PATENTIAL PALM OR FILE Wrapper     SEQ ID NO 332 ; SOFTWARE: PATENTIAL PALM OR FILE WRAPPER     ORGANISM: Homo sapiens     US-09-764-864-332  Query Match     Best Local Similarity 99.4%; Pred. No. 0;     Matches 2028; Conservative 0; Mismatches 8; Indels 4; Gaps 3;     Matches 2028; Conservative 0; Mismatches 8; Indels 1306	Db 2731 TTTATCTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC
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TYPE: DNA
CORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (5)..(1669)
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PRIOR FILING DATE: 2001-10-05
PRIOR PRILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR APPLICATION NUMBER: 60/328,026
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328,849
PRIOR APPLICATION NUMBER: 60/329,414
PRIOR APPLICATION NUMBER: 60/329,414
                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 1624; Conserv
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NUMBER OF SEQ ID NOS: 133
SOFTWARE: CuraSeqList version
SEQ ID NO 39
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/262,445
CURRENT FILING DATE: 2002-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS TITLE OF INVENTION: THE SAME
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OR APPLICATION NUMBER: 60/341,058
OR FILING DATE: 2001-10-22
OR APPLICATION NUMBER: 60/343,629
OR FILING DATE: 2001-10-24
OR APPLICATION NUMBER: 60/349,575
OR FILING DATE: 2001-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2001-10-15
APPLICATION NUMBER: 60/330,142
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Mezes, Peter
Millet, Isabelle
Ooi, Chean Eng
Patturajan, Meera
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Taupier Jr., Raymond
Zerhusen, Bryan
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Zhong, Mei
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nilarity 95.0%;
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Sequence 39, Application US/10262445
Publication No. US20040014058A1
GENERAL INFORMATION:
APPLICANT: Alsobrook II, John
APPLICANT: Burgess, Catherine
APPLICANT: Catterton, Elina
APPLICANT: Chant, John
APPLICANT: Chant, John
APPLICANT: Chandhuri, Amirabha
APPLICANT: Edinger, Shlomit

RESULT 8 US-10-262-445-39

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                                                                                                                                                                                                  Query Match
Best Local Sim
Matches 1145;
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LENGTH: 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Protein
FILE REFERENCE: PTZZ3
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                    OTHER INFORMATION: n e
NAME/KEY: SITE
LOCATION: (774)
OTHER INFORMATION: n e
NAME/KEY: SITE
LOCATION: (777)
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NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE LOCATION: (511
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                                              TCATCATCACCGGGCCACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAAAC 1426
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RESULT 10
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; Sequence 347, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
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APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Henderson, Robert A.

APPLICANT: McNeill, Patricia D.

APPLICANT: Fanger, Neil

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C14

CURRENT APPLICATION NUMBER: US/09/735,705

CURRENT APPLICATION NUMBER: US/09/735,705

CURRENT FILING DATE: 2000-12-12

NUMBER OF SEQ ID NOS: 419
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Fanger, Gary R
Li, Samuel X.
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Fan, Liqun
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GENERAL INFORMATION:

APPLICANT: Kalos, Michael D.

APPLICANT: McNeill, Patricia D.

APPLICANT: McNeill, Patricia D.

APPLICANT: McNeill, Patricia D.

APPLICANT: McNeill, Patricia D.

APPLICANT: Marc W.

APPLICANT: MARC W.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C15

CURRENT APPLICATION NUMBER: US/09/850,716A

CURRENT FILING DATE: 2001-05-07

NUMBER OF SEQ ID NOS: 440

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 347

LENGTH: 1740
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; TYPE: DNA
; ORGANISM: Homo s
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RESULT 12
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APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Peckham, David W.
APPLICANT: Peckham, David W.
ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
ITITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FRASTEEQ for Windows Version 4.0
SEQ ID NO 347
LENGTH: 1740
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                                                            CTGGTTCCCACCCAATTTGTTGGAGCCATCATAGGAAAAGAAGGTGCCACCATTCGGAAC
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Vedvick, Thomas S.
Carter, Darrick
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                                    AAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCAC
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CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 347, Application US/10007700 Publication No. US20030064947A1 GENERAL INFORMATION:
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Best Local Similarity 64.9%;
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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C17
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Li, Samual X.
Kalos, Michael D.
Henderson, Robert A.
McNeill, Patricia D.
Fanger, Neil
Retter, Marc W.
Durham, Margarita
Fanger, Gary R.
Vedvick, Thomas S.
Carter, Darrick
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APPLICANT: Foy, Teresa M.

APPLICANT: Foy, Teresa M.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Watanabe, Yoshihiro

APPLICANT: Henderson, Robert A.

APPLICANT: Kalos, Michael D.

APPLICANT: Kalos, Michael D.

APPLICANT: Spies, Gregory A.

APPLICANT: Fan, Liqun

APPLICANT: Fan, Liqun

APPLICANT: Fan, Liqun

APPLICANT: Wang, Tongtong

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121, 455C18

CURRENT APPLICATION NUMBER: US/10/117,982

CURRENT FILING DATE: 2002-04-05

NUMBER OF SEQ ID NOS: 484

SOFTWARE: FASTSEQ for Windows Version 4.0

TYPE: DNA

ORGANISM: Homo sapiens

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Best Local Similarity 64.9%;
Matches 1116; Conservative
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Pred. No. 1e-179;
0; Mismatches 538;
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                                            AGAGTTATTGGAAAAGGAGGCAAAAACGGTGAATGAACTTCAGAATTTGTCAAGTGCAGAA
                                                                                  CGGGTGATTGGCAAAGGTGGCAAGACCGTGAACGAACTGCAGAACTTAACCAGTGCAGAA 1566
                                                                                                                                   AGTCCTAAAGAAGAGGTGAAACTTGAAGCTCATATCAGAGTGCCATCCTTTGCTGCTGGC
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 478
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Best Local Similarity 64.9%;
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APPLICANT: Kalos, Michael D.
APPLICANT: Mericle, Barbara
APPLICANT: Spies, Gregory A.
APPLICANT: Spies, Gregory A.
APPLICANT: Fan, Liqun
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C18
CURRENT APPLICATION NUMBER: US/10/117,982
CURRENT FILING DATE: 2002-04-05
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Fanger, Gary R.
Vedvick, Thomas S.
Carter, Darrick
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GTTGTAAATGTAACCTATTCCAGTAAGGACCAAGCTAGACAAGCACTAGACAAACTGAAT 420
                                                                   CTAGTCCAGTATGGAGTGGTGGAGAGCTGTGAGCAAGTGAACACTGACTCGGAAACTGCA
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Pred. No. 1e-179;
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1326 1320	TCAAG
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1208	TRACCCCATCACCAGTITGGCCGGTTCCCGCATCATCACTC
1162 1140	1144 CACTCCGGATACTTCTCCA
1143 1080	084 ATAGAGATTATGAAGAAGCTGCGTGAGGCCTTTGAAAATGATATGC
1083	TAA
1023 960	964 AAAATIGAACAIGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCATA
963 900	904 ATCTTGGCACACAATGGCTTGGTTGGAAGACTGATTGGAAAAGAAGGCAGAAATTTGAAG 
903 8 <b>4</b> 0	844 CTTGAAATCATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTGAAA
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Search completed: July 24, 2004, 22:29:09 Job time: 1427.28 secs

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## ALIGNMENTS

PUBMED REFERENCE REFERENCE AUTHORS SOURCE ORGANISM RESULT 1 AK049196 LOCUS ACCESSION VERSION KEYWORDS DEFINITION JOURNAL MEDLINE PUBMED JOURNAL MEDLINE TITLE AUTHORS TITLE Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Komo,H., Okazaki,Y., Muzamatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000) Genome Res. 20499374 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999) Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; AKO49196 3592 bp mRNA linear HTC 20-SEP-2003 Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:C330012H03 product:HEPATOCELLULAR CARCINOMA AUTOANTIGEN bomolog [Homo sapiens], full insert sequence. Mus musculus AK049196.1 GI:26093366 HTC; CAP trapper. AK049196 10349636 Mus musculus (house mouse) Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus cDNAs to genes

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Match 58.9%; Score 1935.2; DB 11; Length 3592; Local Similarity 79.7%; Pred. No. 0;	/clone="0330012H03" /cell_type="ES cells" /clone_lib="RIKEN full-length enriched mouse cDNA library"  34		Encyclopedia Project of Genome Exploration Research Group in Riken Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  Please visit our web site for further details.  URL:http://genome.gsc.riken.go.jp/  URL:http://fantom.gsc.riken.go.jp/.	Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Riken Yokohama (E-mail:genome-res@gsc.riken.go.jp, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, UKL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)	Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojama, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sagabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	Mature 103, 003-030 (2001)  5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  Nature 420, 563-573 (2002)  6 (bases 1 to 3592)  Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,	sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913 11076861 4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection	3 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Yujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayyashizaki,Y. Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayyashizaki,Y. RIKEN integrated sequence analysis (RISA) system384-format
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Mus musculus 6 days neonate head cDNA, RIKEN full-length er
library, clone:5430439D08 product:HEPATOCELLULAR CARCINOMA
AUTOANTIGEN homolog [Homo sapiens], full insert sequence.
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3262)
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Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Subhiro-cho, Tsurumi-ku, Yokoham RIKEN Yokohama (E-mail:genome-res@gsc.riken.go.jp, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9212, Fax:81-45-503-9216)
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URL:http://fantom.gsc.riken.go.jp/
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Eukaryota; Metazoa; Chordata;
Eukaryota; Mutheria; Rodentia;
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2
Carninci, P.,
                                                                                                                              High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                      Carninci, P. and Hayashizaki, Y.
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            Hayatsu, N.,
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            Sugahara, Y., Shibata, K.,
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                   acknowledge.
Please visit our web site for further details
                                                                                                                                                                                                                                                                                                                        URL:http://genome.gsc.riken.go.jp/
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/db xref="FANTOM DB:B130017M24"
/db xref="MGI:2410341"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                  organism="Mus musculus"
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM12753 row: a column: 23
High quality sequence stop: 679.
Location/Qualifiers
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Tissue Procurement: ATCC
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/clone lib="NH1 MGC 88"
/clone lib="NH1 MGC 88"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site_1: Not1; Site_2: Sall; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
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                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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1. (bases 1 to 874)
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                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6207026"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_110"
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AACTGGGTTTTTTGCATACTG
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/note="Organ: pancreas; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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1695 GGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGGCGAGGAAGTGAGGCTCCCCACAGGCA Similarity A--CTGGTTTTTTGCATACTG TGTCACTCCTCATGCCTGTCTAGCTCATACACCCATTTCTCTTTTGCTTCACAGGTTTTAA AGTTCTGGATCACCTGTGTATGTCAACAGAAGGGATACCGTCTCCTTGAAGAGGGAAACTC TTGAGGCCACCCGCACAAAATTCACCCAGAGGGAAATCTCGTCGGAAGGACACTCACGGC TTGAGGCCACCCGCACAAAATTCACCCAGAGGGAAATCTCGTCGGAAGGACACTCACGGC GGCTTTTCTAGACTTTAAAGAATAAAGTCTTTGGGAGGTCTCACGGTGTAGAGAGGAGCT GCAAATCGTCTCTGTACATGTGTGTACATATTAGAAAGGGAAGATGTTAAGATATGTGGC GITGAACTAACATAGGIGAACGIGITCAAAGCCAAGCAAAAIGCACACCCITTITCIGIG 2114 CCAGGITTGCCAGAACCACCGAGCCCCGCCTCCCGCCCCCAGGGCTTCTGCAGGCTTCA GCCAGCCAGATCGGGAGCAAACCAAAGACCATCTGAGGAATGAGAAGTCTGCGGAGGCGG GGCTTTTCTAGACTTTAAAGAATAAAGTCTTTGGGAGGTCTCACGGTGTAGAGAGGAGCT CTGTGGGTTACACAGGGTGCCTGCAGCGGTAATATATTTTAGAAATAATATATCAAATAA GCAAATCGTCTCTGTACATGTGTACATATTAGAAAGGGAAGATGTTAAGATATGTGGC GTTGAACTAACATAGGTGAACGTGTTCAAAGCCAAGCAAAATGCACACCCTTTTTCTGTG GCCATCCACTTCACCATCCACTCGGATCTCTCCTGAACTCCCACGACGCTATCCCTTTTA GCCATCCACTTCACCATCCACTCGGATCTCTCTGAACTCCCACGACGCTATCCCTTTTA CCAGGGACTCTGCCGAGGCCCTGAGAACCCCCAGGGGCCGAGGAGGAGGGGCGGGGAAGGTCAG CCAGGTTTGCCAGAACCACCGAGCCCCCGCCTCCCGCCCCCAGGGCTTCTGCAGGCTTCA GCCAGCCAGATCGGGAGCAAACCAAAGACCATCTGAGGAATGAGAAGTCTGCGGAGGCGG CCAGCAAAACAACGGATGAATGTAGCCCTTCCAACACCTGACAGAATGAGAGCCAAACGCA 1814 GGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGCAGCAAGTGAGGCTCCCACAGGCA CCAGCAAAACAACGGATGAATGTAGCCCTTCCAACACCTGACAGAATGAGACCAAACGCA Conservative 25.7%; 99.4%; 0, Score 842.2; DB 13; Pred. No. 2.3e-154; 0; Mismatches 3; 2553 DB 13; CTTTGCTTCACAGGGTTTAA Indels Length ν, Gaps 2534 1994 2474 2414 2354 2294 2234 2174 1934 780 720 660 600 540 360 2054 300 480 420 1874 120 240 180 1754 60 ۳.

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REFERENCE
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5', mRNA sequence.
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Tissue Procurement: ATCC/DCTD/DTP
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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Location/Qualifiers
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AAGTCAACACAGACACAGAAACCGCCGTTGTCAACGTCACATATGCAACAAGAGAAGAAG
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/lab_host="DH10B (phage-resistant)"
/clone lib="WIH MGC 72"
/note="Organ: Skin; Vector: pCMV-SPORT6;
site_2: Sall; Cloned unidirectionally. P
Average insert size 2 kb. Library const
Technologies."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens cDNA clone IMAGE:6046477
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Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, Fobo, G., Han, M. and Wiemann, S. EST (Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKFZp781G0234_r1 781 (synonym: DKFZp781G0234_5', mRNA sequenc
                                                                                                             No s1 sequence available. This clone (DKFZp781G0234) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                           Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from 5. Wiemann, Molecular Genome Analysis, German Research Center (DKFZ), Email s.wiemann@dkfz- heidelberg. sequenced by Qiagen (Hilden/Germany) within the cDNA sequencentum of the German Genome Project.
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                                               /organism="Homo sapier
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp781G0234"
/dev_stage="adult"
/lab_host="DH10B"
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5', mRNA sequence.
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BQ212500.1 GI:20392787
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/note="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"
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Pred. No. 7.4e-148;
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Mammalia; Eutheria; Primates; Cat
1 (bases 1 to 836)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Ma
Unpublished (1999)
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINI)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LINI at:
http://image.llnl.gov
Plate: LLAM13368 row: n column: 02
High quality sequence stop: 670.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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                                                                                        CTTGAAGAGAAACTCTGTCACTCCTCATGCCTGTCTAGCTCATACACCCATTTCTCTTT
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/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1:
Site_2: Sall; Cloned unidirectionally. Primer:
Average insert size 2 kb. Library constructed
Technologies."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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98.7%;
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Pred. No. 6.2e-146;
0; Mismatches 9;
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Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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                                                              CTACCCCGACCAGAACTGGGCCATCCGCGCCATCGAGACCCTCTCGGGTAAAGTGGAATT
                                  CTACCCCGACCAGAACTGGGCCATCCGCGCCATCGAGACCCTCTCGGGTAAAGTGGAATT
                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: 688.
Location/Qualifiers
                                                                                               Conservative
                                                                                                                                                                         /tissue_type="leiomyosarcoma"
/lab host="DH10B (phage-resistant)"
/clome_lb="NIH_MGC_71"
/clome_tb="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Cyan: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                     organism="Homo sapiens"
                                                                                                                                                                                                                                                                     clone="IMAGE:555652"
                                                                                                                                                                                                                                                                                                                                     .1089
                                                                                                              24.3%;
                                                                                               0;
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Pred. No. 1.6e-145;
0; Mismatches 41;
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                                                                                                                 AGENCOURT 7965128 NIH MGC 72
5', mRNA sequence.
BU156245
      Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 894)
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EST 03-SEP-2002 MAGE:6162660

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TITLE
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Mational Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 666.
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                                                                                          CGTCTCCTTGAAGAGGAAACTCTGTCACTCCTCATGCCTGTCTAGCTCATACACCCATTT
                                                                                                                                                                 TCGTCGGAAGGACACTCACGGCAGTTCTGGATCACCTGTGTATGTCAACAGAAGGGATAC
                                                                                                                                                                                                                                     TCTCACGGTGTAGAGGAGCTTTGAGGCCACCCGCACAAAATTCACCCAGAGGGAAAATC
CTCTTTGCTTCACAGGGTTTAAACTGGTTTTTTGCATACTGCTATATAATTCTCTGTCTC
                           CTCTTTGCTTCACAGGTTTTAAACTGGTTTTTTGCATACTGCTATATAATTCTCTGTCTC
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                                                                       CGTCTCCTTGAAGAGGAAACTCTGTCACTCCTCATGCCTGTCTAGCTCATACACCCATTT
                                                                                                                                           TCGTCGGAAGGACACTCACGGCAGTTCTGGATCACCTGTGTATGTCAACAGAAGGGATAC
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//lab_host="DH10B (phage-resistant)"
/clone_lib="NJH MGC 72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo of Average insert size 2 kb. Library constructed by Life Technologies."
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/mol_type="mRNA"

/db_xref="taxon:9606"
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Pred. No. 3.2e-138;
0; Mismatches 32;
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Library constructed by Life
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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| Homo sapiens cDNA clone IMAGE:4707243
                                                                                                                 Similarity
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/tissue_type="mammary_adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_87"
/clone_lib="NIH_MGC_87"
/clone_sort="CMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT_primed.
Average_insert_size_1.383 kb. Library_enriched_for_full-length_clones_and_constructed_by_Life_Technologies.
Note: this is a NIH_MGC_Library."
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Mammalia; Butheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 940)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                  CD243351
CD243351.1
Email: cgapbs-r@mail.nih.gov
Tissus Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                        Contact: Robert Strausberg, Ph.D.
                                                                   Unpublished (1999)
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plate: NDAM446 row: o column: 04
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High quality sequence stop: 695.
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                                                                   TCACTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAACTCTGGAGCTGCAG
                                                                                                         TGGTCCCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAGAACA
                                                                                                                        TGGTCCCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAGAACA
                                                                                                                                                                  AGAAGCCTGTCACCATCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGCATGATTC
                                                  TCACTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAAGAGAACTCTGGAGCTGCAG
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/lab host="DHIOB-Ton A ( T1 and T5 phage resistances)"
/lab host="DHIOB-Ton A ( T1 and T5 phage resistances)"
/clone lib="NIH_MCC 180"
/clone lib="NIH_MCC 180"
/note="Torgan: Testis; Vector: pCMV-SPORT6.1; Site 1: NotI;
/site 2: EcoRV (destroyed); Library is oligo-dT primed and directionally cloned (BcoRV site is destroyed upon cloning). Average insert size 1.68 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC invitrogen).
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pred. No. 1.4e-136;
0; Mismatches 1;
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Best Local Similarity
Matches 773; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (Dases 1 to 824)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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CF593505.1 GI:36347108
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AGENCOURT 15622249 NIH MGC 147 Homo
IMAGE:30531076 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                     GGCAGCGGAGGAGCCGAGGAGCGCCGGGTACCGGGCCGGGGGAGCCGCGGGCTCTCGGGG
                            AAGAGACGGATGATGAACAAGCTTTACATCGGGAACCTGAGCCCCGCCGCCGTCACCGCCGAC 120
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                                                                                                                                                               Conservative
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31 Rm10A07 Bethesda, MD 20892
                                                                                                                                                                                                                                                      /clone_lib="NIH_MGC_147"
/note="Organ: placenta; Vector: pBluescriptR; Site_1:
all-XhoI; Site_2: BamH; Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: This
a NIH_MGC library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:30531076"
/tissue_type="Human Placenta"
/lab_host="DH108 TonA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                               22.8%;
99.4%;
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                                                                                                                                                         Score 749.8; DB 14;
Pred. No. 2.9e-136;
0; Mismatches 3;
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                DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1677 row: c column: 02
                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                            1 (bases 1 to 889)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, P
                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
BG748346
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                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                       BG748346.1 GI:14058999
                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
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                                                                                                               cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
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TGTCACCATCCATGCCACCCCAGAGGGGACTTCTGAA--GCATGCCGCATGATTCTTGAA
                                                                GCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAACTCTGGAGCTGCAGAGAAAGCC
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/clone="IMAGE:4842553"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 43"
/clone_lib="NIH_MGC 43"
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI, CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. | "
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/mol_type="mRNA"
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IMAGE:6495584 5', mRNA sequence.
BU601634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Procurement: NCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
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                                                                                                                                                                  Similarity
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AAGAGACGGATGATGAACAAGCTTTACATCGGGAACCTGAGCCCGGCGGTCACCGCCGAC 120
                                                                                 GCCAGCCGGAGGAGCGAGCGAGCGGGGTACCGGGGCCGGGGGAGCCGCGGGCTCTCGGGG
                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                               5'-ATTCTAGAGGCCGAGGCGGACATG-dT(30)NN-3'. Full-length enriched library was constructed using the Cloutech Creator SMART kit and size-selected to contain the >0.5 kb size fraction (other fractions present in NIH MGC 141). Library created in the laboratory of M. Brownstein (NIMH, NIH). Note: this is a NIH_MGC Library."
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                                                                                                                                             Score 718.8; DB 13; Pred. No. 3.5e-130; 0; Mismatches 2;
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720 GAACATCACTAAGC 733               727 GAACATCACTAAGC 740	660 GATCCTGGTCCCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAA 719 	601 GAGCAAGGCCACG-CCCCTGGGGGGACTTCTCAGGCCAGACAGATTGATTTCCCGCTGCG 659	541 GAAGAGGTGAGCTCCCCTTCGCCCCCTCAGCGAGCCCAGCGTGGGGACCACTCTTCCCCGG 600	481 GAGAAGCTAAGCGGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCCGGGAT 540 	421 ACAGAAACCGCCGTTGTCAACGTCACATATGCAACAAGAGAAAAAATAGCCAATG 480 	361 TIGGATGGACTITIGGCTCAATAIGGGACAGTGGAGAATGTGGAACAAGTCAACACAGAC 420 	301 AAGCTAAGGAGCAGGAAAATTCAGATTCGAAACATCCCTCCTCACCTGCAGTGGGAGGTG 360 	241 CTCTCGGGTAAAGTGGAATTGCATGGGAAAATCATGGAAGTTGATTACTCAGTCTCTAAA 300 	181 TCCGGCTACGCCTTCGTGGACTACCCCGACCAGAACTGGGGCGATCCGGGCGATCGAGACC 240	121 GACCTCCGGCAGCTCTTTGGGGACAGGAAGCTGCCCCTGGCGGACACGTCCTGCTGAAG 180

Search completed: July 24, 2004, 16:42:45 Job time: 8228.67 secs

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Command line parameters:

MODEL=frame+ n2p.model -DEV=xlp

-Q=/cgn2_1/USETO_spool_p/US09270437/runat_23072004_095738_27403/app_query.fasta_1.5582

-DB=A_Geneseq_29Jan04_-QFMT=fastan_-SUFFIX=rag_-MINMATCH=0.1_-LOOPCL=0

-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human140.cdi

-LIST=45 -DOCALIGN=200 -THR_SCORE=pot -THR MAX=100 -THR_MIN=0 -ALIGN=15

-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000

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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG

-DEV_IIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -KCAPOP=10 -XCAPEXT=0.5 -FGAPOP=6

-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
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Copyright (c) 1993 - 2004 Compugen Ltd
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ABG06795 standard; protein; 594 AA

13-FEB-2002 (first entry)

Novel human diagnostic protein #6786.

Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder.

Homo sapiens.

WO200175067-A2

11-OCT-2001.

30-MAR-2001; 2001WO-US008631

RESULT 1
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XX 31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

HYSEQ INC.

Drmanac RT, Liu C, Tang ΥT

WPI; 200 N-PSDB; 2001-639362/73. DB; AAS70982.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

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             AAGCTAAGCGGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCCGGATGAA
                                                      GluThrAlaValValAsnValThrTyrAlaThrArgGluGluAlaLysIleAlaMetGlu
                                                                   GAAACCGCCGTTGTCAACGTCACATATGCAACAAGAGAAGAAGAAGCAAAAATAGCCATGGAG
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concern. The cancer maybe used in the method may also be of particular use with patient sharing cancer. The method involves comparing the expression level of a marker in a patient sample and the normal level of expression of the marker in a control non-ovarian cancer sample, where the marker is selected from 363 cancer markers described in the control ton. The method of the invention is useful in diagnosing or characterising cancer, in detecting the presence of cancer as early as comparing cancer, in detecting the presence of cancer as early as comparing the patients having an enhanced risk of developing covarian cancer (e.g. patients having an enhanced risk of developing covarian cancer (e.g. patients having a familial history of ovarian concer). The cancer markers may be used in the management and treatment comparing the patients having a familial history of ovarian concer). The cancer markers may be used in the management and treatment comparities, Alzheimer's disease or Parkinson's disease), brain concerning tits, Alzheimer's disease or Parkinson's disease), brain concerning tits, Alzheimer's disease or Parkinson's disease), brain herriations), inflammations (e.g. bacterial or viral meningities or encephalities)
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10-AUG-2001;
19-SEP-2001;
26-SEP-2001;
26-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assessing whether a patient is afflicted with ovarian cancer, useful is assessing the stage or progression of the disease, comprises comparing the expression level of a cancer marker in a sample from a patient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; nontuberculous granulomatous orchitis; connective tissue disorder; heart disorder; schaemic heart disease; atherosclerosis; neoplasm; histological type; carcinogenic; ovarian cancer marker.
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Morrisey MP, Olandt PJ, Sen A, Vi
u K, Schmandt RE, Zhao X, Glatt K;
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멍 Š 멍 Š 밁 Ş 문 Ş В δÃ 뮹 Ş 뫄 δ 뫄 Ş

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

WO200175067-A2

11-OCT-2001

30-MAR-2001; 2001WO-US008631

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

(HYSE-) HYSEQ INC.

RT, Liu ū Ϋ́T;

WPI; 2001-639362/73.

New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

Claim 20; SEQ ID NO 37153; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) creaction (FCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed conditions of (II) or to treat disease states involving (II). (II) is useful in gene therapy techniques to restore normal consistint of (II) or to treat disease states involving (II). (II) is consisted in tissue, as molecular weight markers and as a food conjugation of (II) or distance in the same as a sequence supplement. (II) and its binding partners are useful in medical imaging conjugations and polypurcleotide sequences have applications in conjugation and polynucleotide sequences have applications in conjugation and polynucleotide sequences have applications in conjugation of genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and conjugation acid sequences. AEG00010-AEG30377 represent novel human diagnostic main acid sequences of the invention. Note: The sequence data for this electronic format directly from WIPO at conjugations in the printed specification, but was obtained in flactory published pct\_sequences.

Sequence 614

Best Local Similarity: Query Match: Alignment Percent Similarity: Score: No.: Scores: 1.5e-254 2836.50 92.05% 92.05% 48.19% Gaps: Length: Matches: Mismatches: Indels: Conservative:

US-09-270-437D-8 (1-3283) x ABG06794 (1-614)

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                                            lyLeuAsnLeuSerAlaLeuGlyIlePheSerThrGlyLeuSerValLeuSerProProA
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                                 hePheAlaSerGlnThrAlaGlnArgLysIleArgGluIleValGlnGlnValLysGlnG
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31-JAN-2000; 04-FEB-2000; 24-FEB-2000; 02-MAR-2000; 16-MAR-2000;

2000US-0179065P. 2000US-0180628P. 2000US-0184664P. 2000US-0186350P. 2000US-0189874P.

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13-OCT-2000;
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20-NOV-2000;
21-NOV-2000;
21-NO
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N-PSDB; AAS26150.
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17-MAR-2000;
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2000US-0190076P.
2000US-019123P.
2000US-019133P.
2000US-0205515P.
2000US-0216860P.
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2000US-0231244P.
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N on	Qy 493 GGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCCGGATGAAGAGGTGAGC 552	Qy 433 GTTGTCAACGTCACATATGCAACAAGAGAAGAAGCAAAAATAGCCATGGAGAAGCTAAGC 492	Qy 373 TTGGCTCAATATGGGACAGTGGAGAAATGTGGAACACAGTCAACACACAGACACAGAAACCCCC 432	Qy 313 AGGAAAATTCAGATTCGAAACATCCCTCACCTGCAGTGGGAGGTGTTGGATGGA	Qy 253 GTGGAATTGCATGGAAAATCATGGAAGTTGATTACTCAGTCTCTAAAAAAGCTAAGGAGC 312	Qy 193 TTCGTGGACTACCCCGACCAGAACTGGGGCGATCGGCGCCATCGAGACCCTCTCGGGTAAA 252	Qy 133 CTCTTTGGGGACAGGAAGCTGCCCCTGGCGGGACAGGTCCTGCTGAAGTCCGGCTACGCC 192	Qy 73 ATGAACAAGCTTTACATCGGGAACCTGAGCCCGCCGACCGA	Qy 22 CGCCGGGTACCGGGCGGGGAGCCGGGGGTCTCGGGGAAGAGAGACGGATG 72	x AAU16163 (1-620)	Percent Similarity: 90.78% Conservative: 1  Best Local Similarity: 90.61% Mismatches: 11  Query Match: 47.71% Indels: 46  DB: 4 Gaps: 2	6.82e-252 Length: 2808.00 Matches:	sequence represents a novel secreted protein of the invention. Note: The cc sequence data for this patent did not form part of the printed	CC minerals, cofactors and other nutritional components. The polypeptides can also be used  CC apabilities, fat content, lipid, protein, carbohydrate, vitamins,  CC minerals, cofactors and other nutritional components.	cc can also be used to aid wound healing and epithelial cell proliferation, ct prevent skin aging due to sumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to	CC arrest, cerebrovascular disorders e.g. cardinovascular disorders e.g. cardinovascular disorders e.g. cerebral ischaemia, angiogenesis, CC nervous system disorders e.g. Alzheimer's disease, infections caused by CC bacteria, viruses and fungi and ocular disorders e.g. corneal infection, CC and many other disorders in the contact disorders e.g. corneal infection,	CC immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays CC (ELISA). Disorders which are diagnosed or treated include autoimmune CC diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.	CC rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used CC in diagnosing a pathological condition or susceptibility to a CC pathological condition. Antibodies to the proteins can also be used in	CC encoded secreted proteins. The nucleic acids and proteins are used to CC prevent, treat or ameliorate a medical condition in e.g humans mice
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04 GGCCGGGTGATTGGCAAAGGTGGCAAGACCGTGAACGACTGCAGAACTTAACCAGTGCA 1563 	144 TTTAACCCCAAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCCACAGCT 1503 	8 <b>.4</b>	24 83 I			4.4 23	03	180 1140 383 LeuIleProGlyLeuAsnLeuSerAlaLeuGlyIlePheSerThrGlyLeuSerValLeu 402	3 ATGAAGAAGCTGCGTGAAGCCCTTTGAAAATGATATGCTGGCTG	ω	323 HisGluThrGlyThrLysIleThrIleSerSerLeuGlnAspLeuSerIleTyrAsnPro 342 033 GAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCCTGTGCCAGTTGCTGAGATAGAGATT 1092	303 H18A8nG1YLeuValGLYArgLeuIleGlyLysGluGlyArgAsnLeuLysLysIleGlu 322 973 CATGAAACAGGGACCAAGATAAACAATCTCATCTTTGCAGGATTTTGAGCATATACAACCCG 1032	13 CACAATGGCTTGGTTGGAAGACTGATTGGAAAAGAAGGCAGAAATTTGAAGAAAATTGAA 97	853 ATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTGAAAAATCTTGGGA 912 	793 GTCACCATCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGCATGATTCTTGAAATC 852		673 ACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAGAACATCACTAAG 732 	613 GCCCCTGGGGCACTTCTCAGGCCAGACAGATTGATTTCCCGCTGCGGATCCTGGTCCCC 672	دُ

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The invention relates to human novel polypeptides and their associated complynucleotides. The polypeptides and polynucleotides are useful in gene comply for treating, inhibiting or preventing neural disorders, immune cystem disorders (e.g. systemic lupus erythematosus, rheumatoid arthritis cand multiple sclerosis), muscular disorders, respiratory diseases (e.g. companity estibulitis, masal polyps and sinusitis), reproductive disorders, cardiovascular disorders, cardiovascular disorders, cardiovascular disorders (e.g. congenital heart defects, Ebstein's anomaly and hypoplastic left companity diseases), hyperproliferative disorders (e.g. thoughin's disease and conditions), inflammatory diseases (e.g. septic shock, bursitis and compandicitis), allergic reactions and conditions (e.g. asthma), blood crelated disorders (e.g. thrombosis, atherosclerosis and myocardial confarction) and cancerous diseases. Sequences ABU54914-ABU55699 and conditions and concerns thuman novel polypeptides of the invention
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uProL		yAsni	GAACC	rArgS	GAGCC	32 (1	
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rGlyT	CGGCT	pLeuA:	CTCC	aSerG.			
43 LeuPheGlyAspArgLysLeuProLeuAlaGlyGlnValLeuLeuLysSerGlyTyrAla	ACGCC	rgGln	GGCAG	LyMet	ATG		
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TTCGTGGACTACCCCGACCAGAACTGGGCCATCCGCGCCATCGAGACCCCTCTCGGGTAAA 252

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CACTCCGGATACTTCTCCAGCCTGTACCCCCATCACCAGTTTGGCCCGCTTCCCGCATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes an isolated polypeptide comprising any of 33 90 1273 amino acid sequences (I) given in the specification or its mature form, a sequence that is at least 95 % identical to (I), or a sequence comprising one or more conservative substitutions in the amino acid sequence of (I). The polypeptide is useful for preparing a composition for treating or preventing e.g. cancer. This is the amino acid sequence of a novel human NOV protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alsobrook JP, Burgess CE, Edinger SR, Gerlach VL, Mezes PS, Millet I, Ooi Taupier RJ, Zerhusen BD,
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                                SerCysProSerProProGlnArgAlaGlnArgGlyAspHisSerSerTrpGluGlnGly
                                       AGCTCCCCTTCGCCCCCCAGCGAGCCAGCGTGGGGACCACTCTTCCCGGGAGCAAGGC
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10-JAN-2000;
This invention describes a novel isolated polypeptide (1) which comprising an immunogenic portion of a lung tumor protein or variant (P2) which have cytostatic activity. The polypeptides and polypucleotides are used in compositions and vaccines to inhibit the development of cancer, especially lung cancer, in a patient. Methods described in the invention can be used to monitor the progression of a cancer by carrying out the detection at subsequent time points and comparing the results from the
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                                                                                             Claim
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                                                                            GCAGAGAAGCCTGTCACCATCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGCATG
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              lung tumour; lung cancer; cytostatic;
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                                          recombinant protein sequence SEQ ID NO:446.
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Best Local Similarity:
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12-DEC-2000;
07-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang T,
Mcneill
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15-SEP-2000;
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2000US-00630940.
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The present invention describes human lung tumour proteins. Human lung tumour proteins and polynucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polynucleotides, antibodies, fusior proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABL48959 to ABL49300 and ABB74946 to ABB75070 represent sequences used in the exemplification of the present

Example 2; Page 330-332;

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09-OCT-2000; 2000US-00685696.
12-DEC-2000; 2000US-00735705.
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02-AUG-2000;
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15-SEP-2000;
09-OCT-2000;
12-DEC-2000;
07-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                           The present invention describes human lung tumour proteins. Human lung tumour proteins and polymucleotides have cytostatic and immunostimulant activities, and can be used in vaccine production. Compositions comprising the lung tumour proteins, polymucleotides, antibodies, fusion proteins, T cell populations, or antigen presenting cells that express the lung tumour proteins are useful for treating lung cancer or stimulating an immune response. ABI48959 to ABI49300 and ABB74946 to ABB75170 represent sequences used in the exemplification of the present income.
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   GTGGAATTGCATGGGAAAATCATGGAAGTTGATTACTCAGTCTCTAAAAAAGCTAAGGAGC
                                                                                                                    TTCGTGGACTACCCCGACCAGAACTGGGCCATCGGCGCCATCGAGACCCTCTCGGGTAAA
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Fanger N,
Carter D,
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78.70%
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immune response.
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W, Marnerakis M,
Y, Peckham DW;
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Conservative:
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Fanger GR;
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                                                                                                                                                                                                                                                 LeuTyrAsnProGluArgThrileThrValLysGlyAsnValGluThrCysAlaLysAla
                                                                                                                                                                                                                                                                                                       ATATACAACCCOGAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCCTGTGCCAGTGCT
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                                                                                                                                                                                                                                                                      GCCATCATCGGGAAGAAGAGGGGCACACATCAAACAGCTGGCGAGATTCGCCGGAGCCTCT
                                                                                                                                                 CATCACTCTTATCCAGAGCAGGAGATTGTGAATCTCTTCATCCCAACCCAGGCTGTGGGC
                                                                                                                                                                          {\tt SerGlyMetProProProThrSerGlyProProSerAlaMetThrProProTyrProGln}
                                                                                                                                                                                                                                   ACCCACTCC----
                                                          ATCAAGATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCATCACCGGG
                                                                                              PheGluGln---SerGluThrGluThrValHisLeuPheIleProAlaLeuSerValGly
  TTCTTTAACCCCAAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCCACA 1500
                   ProProGluAlaGinPheLysAlaGinGlyArglieTyrGlyLysIleLysGluGluAsn
                               CCACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAACTGAAAGAGGAAAAC 1440
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The present invention describes isolated human lung carcinoma CC polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic CC activity, and can be used in gene therapy and in vaccines. Compositions CC comprising (I) or (II) can be used for stimulating an immune response in CC a patient and for treating lung cancer in a patient. Oligonucleotides of CI) can be used for detecting the presence of a cancer in a patient, by CC obtaining a biological sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of CC polynucleotide that hybridises to the oligonucleotide and comparing the predetermined cut-off value, and determining the presence of a cancer in CC vaccines. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. ABQ92145 to ABQ9246 and ABP61866 to
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07-MAY-2001;
28-JUN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel lung carcinoma polynucleotide sequences and polypeptides encoded the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Example
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Watanabe Y,
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2001US-00897778.
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abe Y, Peckham DW,
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AAAATCTTGGCACACAATGGCTTGGTTGGAAGACTGATTGGAAAAGAAGGCAGAAATTTG
                                                                                                                                          AACATCACTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAACTCTGGAGCT
                                       IleLeuGluIleMetHisLysGluAlaGlnAspIleLysPheThrGluGluIleProLeu
                                                             ATTCTTGAAATCATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTG
                                                                                   AlaGluLysSerIleThrIleLeuSerThrProGluGlyThrSerAlaAlaCysLysSer
                                                                                                GCAGAGAAGCCTGTCACCATCCATGCCACCCCAGAGGGACTTCTGAAGCATGCCGCATG
                                                                                                                             LeuLeuValProThrGinPheValGlyAlaIleIleGlyLysGluGlyAlaThrIleArg
                                                                                                                                                                                     ATCCTGGTCCCCACCCAGTTTGGTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAG
                                                                                                                                                                                                                 ArgGlnGly---SerProGlySerValSerLysGlnLysProCysAspLeuProLeuArg
                                                                                                                                                                                                                                      {\tt GlnGlnAsnProLeuGlnGlnProArgGlyArgArgGlyLeuGlyGlnArgGlySerSer}
                                                                                                                                                                                                                                                                                                      GGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCCGGATGAAGAGGTGAGC
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                                                                                                                                                                                                                                                                                  TCCCCTTCGCCCCCTCAG-----CGAGCCCAGCGT----
                                                                                                                                                                                                                                                                                                                                              ValValAsnValThrTyrSerSerLysAspGlnAlaArgGlnAlaLeuAspLysLeuAsn
                                                                                                                                                                                                                                                                                                                                                                     GTTGTCAACGTCACATATGCAACAAGAGAAGAAGCAAAAATAGCCATGGAGAAGCTAAGC
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ID ABP61
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XX ABP61
XX APF61
XX O7-OC
XX Humar
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XX Homo
OS Homo
XX WO200
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                                                                                                                               ABP61974;
              WO200247534-A2
                                                       Human; lung cancer;
                                                                              Human lung cancer associated protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCATCATCGGGAAGAAGGGGGCACACATCAAACAGCTGGCGAAGATTCGCCGGAAGCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATCACTCTTATCCAGAGCAGGAGATTGTGAATCTCTTCATCCCAACCCAGGCTGTGGGC 1260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PheGluGln---SerGluThrGluThrValHisLeuPheIleProAlaLeuSerValGly
                                                                                                                                                                                                                        CAGGTGAAGCAGCAGGAGCAGAAA 1704
                                                                                                                                                                                                                                                                                                                 GCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTGATCGTCAGA 1620
                                                                                                                                                                                                                                                                                                                                       AlaGlyArgvalileGlyLysGlyGlyLysThrValAsnGluLeuGlnAsnLeuSerSer
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                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                  (first entry)
                                                                                                                                                     protein;
                                                         lung tumour; cytostatic; gene therapy; vaccine
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                                                                                   SEQ ID NO:449
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Percent Similarity:
Best Local Similarity:
Query Match:

5.47e-165 1875.00 78.70% 64.96% 31.86%

Length:
Matches:
Conservative: Mismatches: Indels:

579 369 78 95 26

US-09-270-437D-8 (1-3283) x ABP61974 (1-579)

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193

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TTCGTGGACTACCCCGAGAACTGGGCCATCCGCGCCATCGAGACCCTCTCGGGTAAA 

40 192 1 MetAsnLysLeuTyrIleGlyAsnLeuSerGluAsnAlaAlaProSerAspLeuGluSer

ATGAACAAGCTTTACATCGGGAACCTGAGCCCGCCGTCACCGCCGACGACCTCCGGCAG

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253

GTGGAATTGCATGGAAAATCATGGAAGTTGATTACTCAGTCTCTAAAAAAGCTAAGGAGC
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IleGluLeuHisGlyLysProIleGluValGluHisSerValProLysArgGlnArgIle

90

60

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 ${\tt TTGGCTCAATATGGGACAGTGGAAATGTGGAACAAGTCAACACAGACACAGAAACCGCC}$ 

81

Score:

Pred. Alignment

No.:

Scores:

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The present invention describes isolated human lung carcinoma compositions (I) and (II) have cytostatic polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic compositions, and can be used in gene therapy and in vaccines. Compositions (I) or (II) can be used for stimulating an immune response in compositions (I) or (II) can be used for stimulating an immune response in the patient of patient and for treating lung cancer in a patient. Oligonucleotides of the obtaining a biological sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of companing that the polynucleotide that hybridises to the oligonucleotide that patient of predetermined cut-off value, and determining the presence of a cancer in the patient. (I) and (II) are useful in pharmaceutical compositions, e.g. the patient. (I) is useful as a marker to indicate the presence or absence of a cancer such as lung cancer. ABQ92145 to ABQ92486 and ABP61866 to the patient sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang T,
Mcneill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-DEC-2000; 2000US-00735705.
07-MAY-2001; 2001US-00850716.
28-JUN-2001; 2001US-00897778.
                                                                                                                                                                                                                                                                                                                                                                                                         Novel lung carcinoma polynucleotide sequences and polypeptides encoded the polynucleotides, useful in pharmaceutical compositions such as vaccines and as markers to indicate the presence of lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Page 375-377; 381pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-583465/62.
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Sequence 579
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Watanabe Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y YAW, Li SX, Kalos MD, Henderson
Retter MW, Durham M, Fanger GR, V
Peckham DW, Cai F, Foy TM;
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CCACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAACTGAAAGAGGGAAAAC
                                                                                   ATCAAGATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCACCGGG
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                                                     PheGluGln---SerGluThrGluThrValHisLeuPheIleProAlaLeuSerValGly
                                                                                                                                                                                                                    CATCACTCTTATCCAGAGCAGGAGATTGTGAATCTCTTCATCCCAACCCAGGCTGTGGGC
                                                                                                                                                                                                                                                                    {\tt SerGlyMetProProThrSerGlyProProSerAlaMetThrProProTyrProGln}
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RESULT 14
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ID ABPG
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Novel lung carcinoma polynucleotide sequences and polypeptides the polynucleotides, useful in pharmaceutical compositions such vaccines and as markers to indicate the presence of lung cancer.

Claim 9; Page 372-374; 381pp; English.

The present invention describes isolated human lung carcinoma polynucleotides (I) and polypeptides (II). (I) and (II) have cytostatic activity, and can be used in gene therapy and in vaccines. Compositions comprising (I) or (II) can be used for stimulating an immune response in a patient and for treating lung cancer in a patient. Oligonucleotides of (I) can be used for detecting the presence of a cancer in a patient, by obtaining a biological sample from the patient, contacting the biological sample with the oligonucleotide, detecting in the sample, an amount of polynucleotide that hybridises to the oligonucleotide and comparing the amount of polynucleotide that hybridises to the oligonucleotide to a predetermined cut-off value, and determining the presence of a cancer in the patient. (I) and (II) are useful in pharmaceutical compositions, e.g.

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21-BUG-2000; 2
15-SEP-2000; 1
12-DEC-2000; 1
07-MAY-2001;
                                                                                                                                                                                                                                                                                              The invention describes isolated polynucleotides and polypeptides useful for diagnosing, preventing and/or treating cancer, particularly lung cancer. A new isolated polynucleotide comprises: any of the 22 fully defined nucleotide sequences (e.g. 1012, 900 or 2773 bp) given in the specification; complements of the nucleotide sequences cited above; at least 10 contiguous residues of the nucleotide sequences cited above; a sequence that hybridise to any of the nucleotide sequences under highly stringent conditions; a sequence that is at least 75 or 90% identical to the above nucleotide sequences, or degenerate variants of the above nucleotide sequences. The composition and methods are useful in diagnosing, preventing and/or treating cancer, particularly lung cancer, in gene therapy and in vaccines. This is the amino acid sequence of a recombinant human lung tumour associated protein.
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Pred. Score:

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Result
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-DB=ISSUEd_Patents_AA_-QFMT=fastan_SUFFIX=rai_-MINMATCH=0.1 -LOOPCI=0
-LOOPEXT=0_-UNITS=bits_START=1 -END=1 -MATRIX=blosum62 -TRANS=human10.cdi
-LIST=45 -DCALIGN=200 -THR_SCORE=pct_-THR_MAX=100 -THR_KIN=0 -ALIGN=15
-MODE-LOCAL_-OUTFMT=pto_-NORM=ext_-HEAPSIZE=500_-MINLEN=0 -MAXLEN=2000000000
-USER=US09270437_GCGN_1 1.59 @runat_23072004_095740_27466_NCPU=6 -ICPU=3
-NO_MMAP_-LARGEQUERY_-NEG_SCORES=0 -WAIT_-DSPBLOCK=100 -LONGLOG
-NO_MMAP_-LARGEQUERY_NEG_SCORES=0 -WAIT_-DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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US-09-480-884A-176
US-09-480-815A-176
US-09-606-4218-176
US-09-606-4218-176
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US-08-726-160-2
US-08-726-160-2
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## ALIGNMENTS

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APPLICANT: ROSS, Jeffrey
TITLE OF INVENTION: THE C-MYC CODING REGION I
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC
FILE REFERENCE: 960296.95131
CURRENT APPLICATION NUMBER: US/09/261,855A
CURRENT FILING DATE: 1999-03-03
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 577
TYPE: PRT
TYPE: PRT
TYPE: PRT
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                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
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GENERAL INFORMATION:
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{\tt SerSerAlaValProProProProSerSerValThrGlyAlaAlaProTyrSerSer}
                                                                                            SerLeuGlnSerHisLeuIleProGlyLeuAsnLeuAlaAlaValGlyLeuPheProAla
                        -TCCAGCCTGTACCCCCATCACCAG
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                            TTTGGCCCGTTCCCGCAT 1200
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US-09-643-597-348
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       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                 Alignment Scores: Pred. No.:
                                                                                                                                                                         APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
TILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILLING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
                                                       Score:
                                                                                                                                     NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 348
LENGTH: 579
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Fanger, Gary R.
Li, Samuel X.
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Fan, Liqun
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Skeiky, Yasir A.W.
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-09-270-437D-8 (1-3283)

x US-09-643-597-348 (1-579)

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   Percent Similarity:
                 Score:
                                     Alignment Scores:
                                                              US-09-542-615A-348
                                                                                                                                           APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
TITLE OF INVENTION: COMPOUNDS AND ME
TITLE OF INVENTION: AND DIAGNOSIS OF
FILE REFERENCE: 210121.45568
CURRENT APPLICATION NUMBER: US/09/542
CURRENT FILING DATE: 2000-04-14
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US-09-542-615A-348
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SOFTWARE: FastSEQ for
SEQ ID NO 348
LENGTH: 579
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                Sequence 348, Application Patent No. 6518256
                                                                        TYPE: PRT
ORGANISM: Homo
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Fan, Liqun
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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
FITTLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FITE REPERENCE: 210121.455C9
CURRENT PILING DATE: 2000-06-28

NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 348
LENGTH: 579
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APPLICANT:
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
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   GENERAL INFORMATION:
APPLICANT: Wang, To
APPLICANT: Wang, To
APPLICANT: Kalos, M
APPLICANT: Bangur,
APPLICANT: Bangur,
APPLICANT: Hosken,
APPLICANT: Fanger,
APPLICANT: Wang, Ai
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NT: Wang, Aijun
NT: Skeiky, Yasir A.W.
NT: Henderson, Robert A.
NT: McNeill, Patricia D.
F INVENTION: COMPOSITIONS A
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Kalos, Michael D.
Bangur, Chaitanya (
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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FILE REFERENCE: 210121.455C11
CURRENT APPLICATION NUMBER: US/09/643,597
CURRENT FILING DATE: 2000-08-21
NUMBER OF SEQ ID NOS: 369
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 176
SEQ ID NO 176
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-480-884A-176
                                  Sequence 176, Application Patent No. 6482597 GENERAL INFORMATION:
       APPLICANT: Wang, Tongtong APPLICANT: Fan, Liqun APPLICANT: Hosken, Nancy
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Alignment S Pred. No.:

US-09-480-884A-176

TYPE: PRT ORGANISM: Homo

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; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CP.
; FILE REFERENCE: 210121.455C6
; CURRENT APPLICATION NUMBER: US/09/480,884A
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSEQ for Windows Version 3.0
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579

"TYDE": DET
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Sequence 176, Application Patent No. 6518256 GENERAL INFORMATION:
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APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy A.
APPLICANT: Hosken, Nancy R.
APPLICANT: Hosken, Nancy R.
APPLICANT: Fanger, Gary R.
ITILE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAN FILE REFERENCE: 210121.455C8
CURRENT PILLING DATE: 2000-04-14
CURRENT FILLING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 350
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 176
LENGTH: 579
TYPE: PAT
ORGANISM: Homo sapiens
US-09-542-615A-176
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APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael
APPLICANT: Bangur, Chaitar
APPLICANT: Hosken, Nancy
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APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND INGROSIS OF LUNG CANCER
FILE REPERENCE: 210121, 455C9
CURRENT APPLICATION NUMBER: US/09/606,421B
CURRENT FILING DATE: 2000-06-28
**TMREP OF SEQ ID NOS: 358
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SOFTWARE: FASTSEQ for Windows Version
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8-021-6 3GAGGTG 	EXEL LINE: HIGO XTURE: THER INFORMATION: Amino Acid 149 (Xaa) is Met 21-608D-2 It Scores: 1.52e-14 Length: 263.50 Matches: Cimilarity: 263.73% Conservative:	FOR SEQ HARACTER 644 MINO ACI NESS: S UNKNC YPE: Pe AL: NO OURCE: Human	; FILING DALE: ; CLASSIFICATION: 435 ; ATTORNEY/AGENT INFORMATION: ; NAME: WILLIAM S. FEILER ; REGISTRATION NUMBER: 26,728 ; REFERENCE/DOCKET NUMBER: 2026-4063 ; TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 758-48800 TELEPHONE: (212) 758-6849	MEDIUM TYPE: EI CORNOTER: IBM EI COPRATING SYSTES SOFTWARE: WORD CURRENT APPLICATIO CURRENT APPLICATION APPLICATION NUM PRIOR APPLICATION PRIOR APPLICATION NUM APPLICATION NUM	P SEQUENCES: NDENCE ADDRES SEE: MORGAN 345 PARK 4345 PARK 10154 10154 READABLE FO	RESULT 9  US-08-021-608D-2 ; Sequence 2, Application US/08021608D ; Patent No. 5580760 ; Patent No. 5580760 ; GENERAL INFORMATION: ; APPLICANT: LEVENS, DAVID L., DUNCAN, ; APPLICANT: ROBERT C., AND AVIGAN, MARK I. ; TITLE OF INVENTION: PROTEIN AND CONA THEREFOR	
QY 1317 CTCTATCAAGATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCATCATCAC 1376	Db 258GINGLYGLYFREATGGILVAL  Qy 1197 GCATCATCACTCTTATCCAGAGCAGGAGATTGTGAATCTCTTCATCCCAACCCAGGCTGT 1256  Qy 1270SerargIleGlyGlyAsnGluGlyIleAspValProIleProArgPheAlaVa 287  Db 270SerargIleGlyGlyAsnGluGlyIleAspValProIleProArgPheAlaVa 287  Qy 1257 GGGCGCCATCATCGGGAAGAAGGGGGCACACATCAAACAGCTGGCGAGATTCGCCCGGAGC 1316	Oy 1032 GGAAAGAACCATCACTGTQAAGGGCACAGTTGAAGGCCTGIGCCAG 1076    :::	TTGAAGAAAATTGA :::  :::::: IleLysGlnLeuGl AGCATATACAACCCGlyPr	Db 136 eAlaProAspSerGlyJLeuProGluArgSerCys***LeuThrGlyThrProGl 155  Qy 816 GGGGACTTCTGAAGCATGCCGCATGATTCTTGAAAATCATGCAAAAAAAA	636 97 696 116	516 CTTCAAGATTTCCTACATCCCGGATGAAGAGTGAGCTCCCCTTCGCCCCCTCAGCGAGC :::	Qy 396 GAATGTGGAACAAGTCAACACAGAAAACCGCCGTTGTCAAACGTCAACTATATGCAAC 455

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RESULT 10
US-08-726-160-2
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                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                         COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                     APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
                                                                          APPLICATION NUMBER: US/08/726,160
FILING DATE: 04-OCT-1996
   CLASSIFICATION:
                  APPLICATION NUMBER: FILING DATE: 22-FE
                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                            CITY: NEW YORK
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               22-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No.:
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION:
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NAME: WILLIAM S. FEILER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: Amino Acid
STRANDEDNESS: Sin
TOPOLOGY: Unknown
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CELL LINE: HL60
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 oGlyPheHisHisGlyAspGlyProGlyAsnAlaValGln----
                                                           uSerValGlnSerAlaLysArgLeuLeuAspGlnIleValGluLysGlyArgProAlaPr
                                                                                           GGGGACTTCTGAAGCATGCCGCATGATTCTTGAAATCATGCAGAAA-----
                                                                                                                           e---AlaProAspSerGlyGlyLeuProGluArgSerCys***LeuThrGlyThrProGl
                                                                                                                                                          eGlyArgGlyGlyGluGlnIleSerArgIleGlnGlnGluSerGlyCysLysIleGlnIl
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Matches:
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1803 AGACCAAACGCAGCCAGACCGGAACCAAACCCAAAGACCATCTGAGGAATGAGAAGT 1862     482 GlyProTyrAsnProAlaProTyrAsnProGlyPro		1633TTCTTTGCTAGCCAGACTGCACAGCGCAAGATCAGGGAAATTGTACAACA 1682 :::		1458 AGAAGTGAAGCTGGAAGCGGALALCANGIGCCCLICCACCACCACCACCACCACCACCACCACCACCACCACCA		8 6 1G1			2/0  1257 GEGEGGCATCATCAGAAAAGAGGGGCACAAACAACAGCTGGCGAGATTCGCCGGAGC 1316  1257 GGGCGCCATCATCAGAAAAGAGGGGCACAAACAACAGCTGGCGAGAGTTCGCCGGAGC 1316	GCATCATCACTCTTATCCAGAGCAGGAGATTGTGA	1137 TAACACCCACTCCGGATACTTCTCCAGCCTGTACCCCCCATCACCAGTTTGGCCCGTTCCC 1196	1077 TGCTGAGATAGAGATTATGAAGAAGCTGCGTGAGGCCTTTGAAAATGATATGCTGGCTG	GGAAAGAAGA GGAAAGAAGA 		912 ACACAATGGCTTGGAAGACTGATTGGAAAAGAAGGCAGAAATTTGAAGAAAATTGA 971
Alignment Scores: 1.52e-14 Length: 644 Pred. No.: 263.50 Matches: 140 Score: 263.50 Matches: 86 Percent Similarity: 37.73% Conservative: 86	PEATURE:  NAME/KEY:  LOCATION:  IDENTIFICATION METHOD:  OTHER INFORMATION:  OTHER INFORMATION: Amino Acid 149 (Xaa) is Met or Ile  PCT-US94-01782-2	; HAPLOTYPE: ; TISSUE TYPE: ; CELL LINE: HL60 ; ORGANELLE:	ORIGINAL SOURCE: ORGANISM: Human STRAIN: INDIVIDUAL ISOLATE: DEVELOPMENTAL STAGE:	; LENGTH: 644 ; TYPB: Amino Acid ; STRANDEDNESS: Single ; TOPOLOGY: Unknown ; MOLECULE TYPE: Peptide/Protein ; HYPOTHETICAL: No	; TELECOMMUNICATION INFORMATION: ; TELEPHONE: (212) 751-6849 ; TELEPAX: (212) 751-6849 ; INFORMATION FOR SEQ ID NO: 2: ; SEQUENCE CHARACTERISTICS:	OCK	CLASSIFICATION: ; PRIOR APPLICATION DATA: ; APPLICATION NUMBER: U.S. 08/021,608 ; PILING DATE: 22-FEB-1993	WORDPERF LICATION D N NUMBER: TE: 22-FF	; ZIP: 10154 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: FLOPPY DISK ; COMPUTER: IBM PC COMPATIBLE . OPERATING SYSTEM: PC-DOS/MS-DOS	TRY: USA	NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSEE: MORGAN & FINNEGAN CORRESPO. 145 PARK AVENUE	AS HE <i>F</i> NVENI	PCT-US94-01782-2 PCT-US94-01782-2 ; Sequence 2, Application PC/TUS9401782 ; GENERAL INFORMATION: ; GENERAL INFORMATION: THE GOVERNMENT OF THE UNITED STATES	1920 GGCGGGAAGGTCAGCCAGGTTTGCCAGAACHACCHARACTCCCACCHACHACACTCACCHACHACACTCACCHACHACACTCACCHACHACACTCACCHACHACACTCACCHACHACACTCACCHACHACACTCACCHACHACACTCACACCTCACCTACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTCACCTACACCTACACCTCACCTCACCTACACCTAC	  yPro

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Qy 1077 TGCTGAGATAGAGATATGAAAAGCTGCGTGAGGCCTTTGAAAATGATATGCTGGCTG	155 862 175 912 192 972 972 212 213	·- ·	Best Local Similarity: 23.37% Mismatches: 237  Query Match: 4.48% Indels: 136  DB: 25  US-09-270-437D-8 (1-3283) x PCT-US94-01782-2 (1-644)  Qy 336 CCCTCCTCACCTGCAGTGGGAGGTGTTGGATGGACTTTTGGCTCAATATGGGACAGTGGA 395
FARENT NO. 5580760  GENERAL INFORMATION: APPLICANT: LEVENS, DAVID L., DUNCAN, APPLICANT: ROBERT C., AND AVIGAN, MARK I.  TITLE OF INVENTION: NOVEL FUSE BINDING INTELS OF INVENTION: NOVEL FUSE BINDING INVENTION: NOVEL FUSE BINDING INVENTION: NOVEL FUSE BINDING INVENTION: NOVEL FUSE BINDING INVENTION: NOVEL FUSE BINDING INVENTION: NOVEL FUSE BINDING INVENTION: NOVEL FUSE INVENTION: NOVEL FUSE INVENTION: NOVEL FUSE INVENTION: NAME OF INVENTION INVENTION: NAME OF INVENTION INVENTION: NAME OF INVENTION INV	180 180 186 196 192 192	1518 CAAAGGTGGCAAGACCGTGAACTGCAGAACTTAACCAGTGCAGAAGTCATCGTGCCCCAGAAGTCATGCAGAAGTCATCGTGCCCCCAGAAGTGCAAAGTCATCGTGCCCCCAGAAGTGCAAAGTCATCGTGCCCCCAGATGAAACTCATGAAAGTCATGAAAATGAAATTGATCAGGCAACCCCAGATGAAAAATGAAGAAGTGAATCGTCAGAAATTATCGGGCAC	Qy 1317 CTCTATCAAGATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCATCAC 1376    :::      :::

Alignment Scores:  Pred. No.:  262.00  Matches:  140  Percent Similarity:  23.378  Best Local Similarity:  23.378  Best Local Similarity:  23.378  Best Local Similarity:  23.378  Best Local Similarity:  23.378  Best Local Similarity:  23.378  Best Local Similarity:  23.378  Best Local Similarity:  25  Best Local Similarity:  25  Best Local Similarity:  25  Best Local Similarity:  25  Best Local Similarity:  27  Best Local Similarity:  27  Best Local Similarity:  28  Best Local Similarity:  29  36 CCCCCCCCCCACCTGOAGTGACAGTCACCAGACACACACACACACACACACACACA	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPEREECT 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/O8/021,608D FILING DATE: 22-FEB-1993 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE: CLASSIFICATION NUMBER: CLASSIFICATION NUMBER: 26,728 REFERENCE/DOCKET NUMBER: 2026-4063 TELECOMMUNICATION INFORMATION: TELEPAX: (212) 751-6849 INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 643 TYPE: Amino Acid STRANDENNESS: Single TOPOLOGY: Unknown MODLECULE TYPE: Peptide/Protein HYPOTHETICAL: NO ORIGINAL SOURCE: ORIGINAL SOURCE: ORIGINAL SOURCE: OTHER INFORMATION: Amino Acid 148 (Xaa) is Met or Ile US-08-021-608D-10
\$ \$\text{\$\ext{\$\text{\$\exittitt{\$\text{\$\exittit{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\text{\$\	\$\frac{1}{2}\$ \frac{1}{2}\$ \fra
	816 GGGGACTTCTGAAGCATGCCGCATGATTCTTGAAATCATGCAGAAA

Alignment Scores: Pred. No.: 2.06e-14 Length: 643 Score: 262.00 Matches: 140	US-08-726-160-10 Amino Acid 148 (Xaa) is Met or Ile	LINE: HL60	<pre>/ MOLECULE TYPE: Peptide/Protein / HYPOTHETICAL: No / ORIGINAL SOURCE: / ORGANISM: Human</pre>	; TYPE: Amino Acid ; STRANDEDNESS: Single ; TOPOLOGY: Unknown	E CHARACTERISTICS: H: 643	TELEPHONE: (212) 758-48400 TELEFAX: (212) 751-6849 INFORMATION FOR SEQ ID NO: 10:	들었다.	CLASSIFICATION: 4355 ATTORNEY/AGENT INFORMATION: NAME: WILLIAM S FETTER	3 5	FILING DATE: 004-0CT-1996 CLASIFICATION: 435	CURRENT APPLICATION DATA: APPLICATION NIMBER: 116/08/726 160	NG S	S E E	CITY: NEW YORK STATE: NEW YORK COUNTRY. HISA	ADDRESSEE: MOGAN & FINNEGAN STREET: 345 PARK AVENUE	OVEL FUSE BINDING ROTEIN AND CDNA TE 24	NERAL APPLIC	US-08-726-160-10  US-08-726-160-10  Sequence 10, Application US/08726160	Db 509 TrpGlyAsnAlaTyrProHisTrpGlnGlnAlaProProAspProAla 525	1920 GGCGGGAAGGTCAGCCAGGTTTGCCAGAACCACCGAGCCCCGCC 1964	Db 493ProGlyProAlaProHisGlyProProAlaProTyrAlaProGlnGy 508	481 GlyProTyrAsnProAlaProTyrAsnProGl	1803	Qy 1743 CTCCCACAGGCACCAGCAAAACAACGGATGAATGTAGCCCTTCCAACACCTGACAGAATG 1802
Db 269SerargIleGlyGlyAsnĠluGlyIleAspValProlleProArgPheAlaVa 286  Qy 1257 GGGCGCCATCATCGGGAAGAAGGGGGCACACATCAAACAGCTGGCGAGATTCGCCGGAGC 1316       :::      :::          ::::::	1197 GCATCAT	QY 1137 TAACACCCACTCCGGATACTTCTCCAGCCTGTACCCCCATCACCAGCTTTGGCCCGTTCCC 1196	<u>.</u>	225 odlnAsnThrGlyAlaAspLysProLeuArgIleThrGlyAspProTyrLysValGlnGl	FTTGAGGCCTGTGCCAG	QY 972 ACATGAAACAGGGACCAAGATAACAATCTCATCTTTTGCAGGATTTGAGCATATACAACCC 1031 :			QY 862GAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTGAAAATCTTGGC 911	154	816 GGGGACTTCTGAAGCATGCCCCATGATTCTTCTAAAATGCTATGCTATGATTCTTCTAAAGCATGCTATGATTCTTCTAAAATGCTATGCTATGATTCTTCTATGATTCTTCTATGCTATGATTCTTCTATG	Þ			636	Db CHAGCGIGGGGACCACTCTTCCCGGGAGCAAGGCCACGCCCCTGGGGGCACTTCTCAGGC 635	5 9 6		TTTGAGAACTACTC				(1-643)	Percent Similarity: 37.56% Conservative: 85  Best Local Similarity: 23.37% Mismatches: 237  Query Match: 4.45% Indels: 137  DB: 1 Gaps: 25

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Sequence 10, Application:
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ADDRESSEE: MORGAN &
STREET: 345 PARK AVE
                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                           STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1920 GGCGGGAAGGTCAGCCAGGTTTGCCAGAA-----CCACCGAGCCCCGCC 1964
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                                                             10154
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                                                                                                                                                                                            345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                     THE GOVERNMENT OF THE UNITED STATES
AS REPRESENTED BY THE SECRETARY, DEPARTMENT
HEALTH AND HUMAN SERVICES
IVENTION: NOVEL FUSE BINDING
IVENTION: PROTEIN AND CDNA THEREFOR
                                                                                                    USA
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Best Local Similarity:
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REGISTRATION NUMBER: 26,728
REFERENCE DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-6840
TELEPAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 10:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/0178
FILING DATE: 22-FEB-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: Unknow MOLECULE TYPE: Per HYPOTHETICAL: NO ORIGINAL SOURCE:
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APPLICATION NUMBER: U.S.
FILING DATE: 22-FEB-1993
ATTORNEY/AGENT INFORMATION:
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 No.:
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IDENTIFICATION METHOD:
OTHER INFORMATION: Am.
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STRANDEDNESS: Sir
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RESULT 14 PCT-US94-01782-10

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  TCGTGACCAAACGCCAGATGAAAATGAGGAAGTG---ATCGTCAGAATTATCGGGCAC--
                                                                                    CARAGGTGGCAAGACCGTGAACGAACTGCAGAACTTAACCAGTGCAGAAGTCATCGTGCC
                                         yLysGlyGlyGluThrIleLysSerIleSerGlnGlnSerGlyAlaArgIleGluLeuGl 412
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                                                                                                                                                                     TELEFAX: (212) 751-6849 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THER
NUMBER OF SEQUENCES: 24
                  MOLECULE TYPE: PORTHETICAL: NO
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 22-FEB-
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA
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ADDRESSEE: MORGAN & FINNEGAN
                                                           TOPOLOGY:
                                                                           TYPE: Amino Acid
STRANDEDNESS: Sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                              TELEPHONE:
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; ORGANISM:
; CELL LINE:
US-08-021-608D-8
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-270-437D-8 (1-3283) x US-08-021-608D-8 (1-590)
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                                                                                                                                                                                                  1288 АТСАЛАСАGCTGGCGAGATTCGCCGGAGCCTCTATCAAGATTGCCCCTGCGGAAGGCCCA 1347
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341 GlyGlyArgGlyArgGlyArgGlyGlnGlyAsnTrpAsnMetGlyProProGlyGlyLeu 360
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|GlnIleValGluLysGlyArgProAlaProGlyPheHisHisGlyAspGlyProGlyAsn 169
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|leThrGlyAspProTyrLysValGlnGlnAlaLysGluMetValLeuGluLeuIleArg 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---IleGlnAsp------GlyProGlnAsnThrGlyAlaAspLysProLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTTTGCAGGATTTGAGCATATACAACCCCGGAAAGAACC-----ATCACT 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGAAGGGCACAGTTGAGGCCTGTGCCAGTGCTGAGATAGAGATTATGAAGAAGCTGCGT 1107
                                                        GluIleIleThrAspLeuLeuArgSerValGlnAlaGlyAsnProGlyGlyProGlyPro 340
                                                                                                               ThrThrProGluArgIleAlaGlnileThrGlyProProAspArgCysGlnHisAlaAla 320
                                                                                                                               GACGTCAGCGAAAGGATGGTCATCATCACCGGGCCACCGGAA---GCCCAGTTCAAGGCC 1404
                                                                                                                                                                       ileLysLysIleGlnAsnAspAlaGlyValArgileGlnPheLysProAspAspGly---
                                                                                                                                                                                                                                                                                   -----ArgAsnGluTyrGly-------SerArgIleGlyGlyAsnGluGly 261
                               ---GGACGGATCTTTGGGAAA--
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HL60
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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504 lnAlaProProAspProAla 510	Db	
1950CCACCGAGCCCCGCC 1964	Qy 1	
484 lybroProAlabroTyrAlabroGlnGlyTrpGlyAsnAlaTyrProHisTrpGlnGlnG 504	Дb	
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463ThrProMetGlyProTyrAsnProAlaProTyrAsnProG 476	Db	
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448 GlyVal-ProGlyProHisGlyProProGlyProProGly-ProGly 462	Db	
ACGGATGA	Qy 1	
428 GluGluLysileGlyGlyProValAsnProLeuGlyProProValProHisGlyProHis 447	Ф	
	Qy 1	
408 MetLysLeuPheThrileArgGlyThrProGlnGlnIleAspTyrAlaArgGlnLeuIle 427	Db .	
	Qy 1	
388 GlnGlnSerGlyÅlaArgIleGluLeuGlnArgAsnProProProAsnAlaAspProAsn 407	Db	
1549 AACTTAACCAGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAA 1608	0y 15	
368 ProThrGlyLysThrGlyLeuIleileGlyLysGlyGlyGluThrIleLysSerIleSer 387	Db 3	
	Qy 14	
361 GlnGlubheAsnPheIleVal 367	Db 3	
1429 AAAGAGGAAAACTTCTTTAACCCCCAAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTG 1488	Оу 14	

Search completed: July 23, 2004, 11:20:10 Job time : 65.5087 secs

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Result
No.
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-VC=/cgr2 1/USPTO_spool_p/US09270437/runat_23072004_095742_27560/app_query.fasta_1.5582
-DB=Published_Applications_AA -QFMT=fastan_-SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEX=2000000000 -USER-US09270437 @CGN 1 1 35 @runat 23072004 095742_27560
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       number of hits satisfying chosen parameters:
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        Query
Match Length
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , I
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13126.119 Million cell updates/sec
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/ (gn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/ (gn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/ (gn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/ (gn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/ (gn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
/ (gn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/ (gn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2
            ВB
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7.0
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Description
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ALIGNMENTS

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RESULT 1
US-10-097-340-147
; Sequence 147, Application US/10097340
; Publication No. US20030087250A1
; Publication No. US20030087250A1
; GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Sebastian HOERSCH
APPLICANT: Sebastian HOERSCH
APPLICANT: Stave G. KOVATS
APPLICANT: Michael MORRISEY
APPLICANT: Michael MORRISEY
APPLICANT: Michael MORRISEY
APPLICANT: Mobert C. BAST,
APPLICANT: Robert C. BAST,
APPLICANT: Robert C. BAST,
APPLICANT: Karen LU
APPLICANT: Karen LU
APPLICANT: Karen GLATT
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
FILE REFERENCE: MRI-030
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-25,149
PRIOR APPLICATION NUMBER: 60/25,149
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR APPLICATION NUMBER: 60/274,967
PRIOR FILING DATE: 2001-03-14
PRIOR PILING DATE: 2001/09/26
PRIOR PILING DATE: 2001/09/26
PRIOR PILING DATE: 2001/09/26
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR APPLICATION NUMBER: 60/323,102
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FASSEQ for Windows Version 4.0
SEQ ID NO 147
LENGTH: 556
                                                                                                                                                                                                                                                                        US-09-270-437D-8 (1-3283) x US-10-097-340-147
                                                                                                                                                                                                                                                                                                                        Pred. No.:
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; ORGANISM: Homo
US-10-097-340-147
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SerSerProSerProGlnArgAlaGlnArgGlyAspHisSerSerArgGluGlnGly
                                                     AGCTCCCCTTCGCCCCCCAGCGAGCCAGCGTGGGGAACCACTCTTCCCGGGAAGCAAGGC
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100.00%
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Matches:
Conservative:
Mismatches:
Indels:
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US-10-648-593-182
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SEQ ID NO 182
LENGTH: 556
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TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS OF TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OI TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
FILE REFERENCE: D0273 NP
CURRENT FAPLICATION NUMBER: US/10/648,593
CURRENT FILING DATE: 2003-08-26
PRIOR APPLICATION NUMBER: 60/406,385
PRIOR APPLICATION NUMBER: 60/406,385
PRIOR FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 557
NUMBER OF SEQ ID NOS: 557
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                                                                                                                                     SerGlyHisGlnPheGluAsnTyrSerPheLysIleSerTyrIleProAspGluGluVal
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 CCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAGAACATCACT
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APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1116
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NAME/KEY: SITE
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OTHER INFORMATION: 1
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PILE REFERENCE: 21402-462D

CURRENT FILING DATE: 2002-10-01

CURRENT FILING DATE: 2002-10-01

PRIOR APPLICATION NUMBER: 60/327,454

PRIOR FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: 60/327,917

PRIOR APPLICATION NUMBER: 60/328,029

PRIOR APPLICATION NUMBER: 60/328,029

PRIOR FILING DATE: 2001-10-09

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PRIOR PILING DATE: 2001-10-09

PRIOR APPLICATION NUMBER: 60/328,056

PRIOR PILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: 60/328,449

PRIOR APPLICATION NUMBER: 60/329,414

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PRIOR APPLICATION NUMBER: 60/330,142

PRIOR APPLICATION NUMBER: 60/330,142

PRIOR APPLICATION NUMBER: 60/341,058

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PRIOR PILING DATE: 2001-10-22

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PRIOR APPLICATION NUMBER: 60/343,629

PRIOR PILING DATE: 2001-10-24

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APPLICANT: Alsobrook II, John
APPLICANT: Burgess, Catherine
APPLICANT: Catterton, Elina
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Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 133
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 40
LENGTH: 555
TYPE: PRT
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TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND
TITLE OF INVENTION: THE SAME
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                                                                    PRIOR APPLICATION NUMBER: 60/349,575 PRIOR FILING DATE: 2001-10-29
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GENERAL INFORMATION:

APPLICANT: MCNAbb, Andria
APPLICANT: MCNAbb, Andria
APPLICANT: McNabb, Andria
APPLICANT: McNabb, Andria
APPLICANT: Watanabe, Yoshihhiro
APPLICANT: Watanabe, Yoshihhiro
APPLICANT: Wang, Tongtong
ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C19
CURRENT APPLICATION NUMBER: US/10/313,986
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 500
LENGTH: 577
TYPE: PRT
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US-10-313-986-500
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                  ORGANISM: Homo
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APPLICANT: Ross, Jeffrey
APPLICANT: Ross, Jeffrey
TITLE ON INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN
TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE
FILE REFERENCE: 960296.95131
CURRENT APPLICATION NUMBER: US/09/873,637
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 577
TYPE: PRT
ORGANISM: Mus musculus
S-09-873-637-2
                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09873637
Patent No. US20020061543A1
GENERAL INFORMATION:
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GENERAL INFORMATION:

APPLICANT: MCNAbb, Andria
APPLICANT: MCNAbb, Andria
APPLICANT: MCNAbb, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C19
CURRENT APPLICATION NUMBER: US/10/313,986
CURRENT FILING DATE: 2002-12-04
NUMBER OF SEQ ID NOS: 560
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 486
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Publication No. US20030236209A1
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RESULT 9
US-09-735-705-348
                           GENERAL INFORMATION:
APPLICANT: Wang, To
APPLICANT: Fan, Liq
APPLICANT: Kalos, MAPPLICANT: Bangur,
                                                                               Sequence 348, Application US/09735705 Patent No. US20020052329A1
          APPLICANT:
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Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Panger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER TITLE REFERENCE: 210121.455C14
CUBRENT APPLICATION NUMBER: US/09/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
NUMBER OF SEQ ID NOS: 419
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Skeiky, Yas
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                                     GlnValLysGlnHisGlnGlnGln 566
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SOFTWARE: FastSEQ for Windows Version
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LENGTH: 579
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APPLICANT: Kalos, Michael D.
APPLICANT: McNeill, Patricia
APPLICANT: Retter, Marc W.
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CURRENT APPLICATION NUMBER: US/09/850,716A
CURRENT FILING DATE: 2001-05-07
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APPLICANT: Catter, Darrick
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CURRENT APPLICATION NUMBER: US/09/897,778
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 446
LENGTH: 579
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-897-778-446
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Carter, Darrick
Ratanabe, Yoshihiro
Robert A.
GGGCATCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCCGGATGAAGAGGTGAAGCCC
                                                                   GTTGTCAACGTCACATATGCCAACAAGAGAAGAAGCAAAAAATAGCCATGGAGAAGCTAAGC
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Peckham, David W.
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THE
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C16
CURRENT APPLICATION NUMBER: US/09/897,778
CURRENT FILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 467
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 449
LENGTH: 579
TYPE: PRT
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Best Local Similarity:
Query Match:
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APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Marnerakis, Mai
APPLICANT: Marnerakis, Mai
APPLICANT: Vedvick, Thomas
APPLICANT: Carter, Darrich
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Vedvick, Thomas S.
Carter, Darrick
       Watanabe, Yoshihiro
Henderson, Robert A
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       ProProGluAlaGlnPheLysAlaGlnGlyArgIleTyrGlyLysIleLysGluGluAsn
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CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 348
LEUGTH: 579
TYPE: PRT
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APPLICANT: Foy, Teresa M.
APPLICANT: Foy, Teresa M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121,455C17
FILE REFERENCE: 120121,455C17
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Retter, Marc W.
Durham, Margarita
Fanger, Gary R.
Vedvick, Thomas S.
Carter, Darrick
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Peckman, David W.
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                                                                                                        APPLICANT: FOY, Teresa M.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C17
CURRENT PAPLICATION NUMBER: US/10/007,700
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 579
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Vedvick, Thomas S.
Carter, Darrick
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                   AAGAAAATTGAACATGAAACAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGC 1020
                                             LysileLeuAlaHisAsnAsnPheValGlyArgLeuIleGlyLysGluGlyArgAsnLeu
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## ALIGNMENTS

밁 Ś 맑 Ś US-09-270-437D-8 (1-3283) x T23837 (1-854) Percent Similarity:
Best Local Similarity:
Query Match: A;Map position: 3 A;Introns: 38/3; 96/1; 133/3; 255/3; A; Molecule type: DNA A; Residues: 1-854 <WIL> A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA R;Sulston, J. submitted to the EMBL Data Library, hypothetical protein M88.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999 C;Accession: T23837 Alignment Scores: A; Gene: CESP: M88.5 A; Experimental source: clone A; Cross-references: EMBL: Z34802; A;Reference number: Z19806 A;Accession: T23837 Score ;Genetics: No.: 264 GlnGlnHisGlnAlaGlyGlnHisGlnGerHisHisGlnSerGlnAsnHisAsn---460 GAAGAAGCAAAAATAGCCATGGAGAAGCTAAGCGGGCATCAGTTTGAGAACTACTCCTTC 519 422 CAGAAACCGCCGTTGTCAACGTCACATATGCAACAAGA---GinHisProGlnMetMetGlnGlnHisAlaGlnGlnGlyTyrHisProHisGlnGlnAsn 1.48e-24 474.50 40.17% 25.71% 8.06% M88 PIDN: CAA84338.1; GSPDB: GN00021; CESP: M88.5 June 1994 307/3; 395/2; Gaps: Length: Matches: Mismatches: Indels: Conservative: 436/2; 492/3; 657/3; 759/1; 820/1 854 153 86 176 181 263 459

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10 45	1027 AACCCGGAAAGAACC
1 439	DAGGGACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCAT          
1 966	907 TTGGCACACAATGGCTTGGTTGGAAGACTGATTGGAAAAGAAGGCAGAAATTTGAAGAAA
403	853 ATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTGAAAATC :::
383	793 GTCACCATCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGCATGATTCTTGAAATC :::   :::
792	748 GTAGATATCCATAGAAAAGAGAACTCTGGAGCTGCAGAGAAGCCT        ::: ::       344 ValAspPheValAsnLeuSerLysLysGluArgThrValLeuGlyAsnAsnAspArgIle
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	Approximation: 5  A;Introns: 181/3; 340/3; 535/2  Alignment Scores: 8.58e-11 Length: 611 Score: 274.00 Matches: 118 Score: 274.00 Matches: 79 Best Local Similarity: 24.63* Mismatches: 183 Query Match: 2 Gaps: 18  US-09-270-437D-8 (1-3283) x T19217 (1-611)  Qy 667 GTCCCACCAGGTTGGTGGGCATAAAGAAGAAGACATC 726 ::	RESULT 3 T19217 hypothetical protein C12D8.1b - Caenorhabditis elegans C,Species: Caenorhabditis elegans C,Species: Caenorhabditis elegans C,Species: Caenorhabditis elegans C,Accession: T19217 R,McMurray, A. submitted to the EMBL Data Library, June 1996 A;Reference number: Z19092 A,Recession: T19217 A,Status: preliminary; translated from GB/EMBL/DDBJ A,Mclecule type: DNA A,Residues: 1-611 <wild- a,experimental="" b,carocal="" b,carola="" c,<="" c,carola="" c,generics:="" c12d8="" carola="" clone="" source:="" td="" the="" to=""><td>Db 394</td></wild->	Db 394

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           GlnThrAlaAlaProAlaAlaAlaProTyr-AlaAlaAlaGlyIleValGlnPro
                                                                                                                                                GAAGAAGTGAAGCTGGAAGCG-----CATATCAGAGTGCCCTCTTCCACAGCTGGC
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                                                                                                                                                                                       GGAGCAAACCAAAGACCATCTGAGGAATGAGAAGTCTGCGGAGGCGGCCAGGGACTCTGC
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                                              AACCACCGAGCCCCGCCCCCCCCCCAGGCCTTCTGCAGGCTTCAGCCATCCA
                                                                                                                 -----ValProArgSerSerValGlyIleIleIleGlyLysGlnGlyAspThrIleLys
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hypothetical protein F8M21.160 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000 C;Accession: T49962 R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; submitted to the Protein Sequence Database, April 2000 A;Reference number: Z24493 A;Accession: T49962 A;Accession: T49962
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A;Residues: 1-568 <BEV>
A;Residues: 1-568 <BEV>
A;Cross-references: EMBL:AL353993; GSPDB:GN00063; ATSP:F8M21.160
A;Experimental source: cultivar Columbia; BAC clone F8M21
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                                          ATCACTGTGAAGGGCACAGTTGAGGCCTGTGCCAGTGCTGAGATAGAGATTATGAAGAAG 1101
                                                                                                                             AAGATAACAATCTCATCTTTGCAGGATTTGAGCATA----TACAACCCGGAAAGAACC 1041
                                                                                                                                                                      GlyCysIleLeuGlyArgGlyGlyGlnIleValGlnAsnIleArgSerGluThrGlyAla
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GlnIleArgIleValLysAspArgAsnMetProLeuCysAlaLeuAsnSerAspGluLeu 198
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                                         rSerProTyrGlyAlaProValGly 546
                                                                                       AGCCCGCCTCCCGCCCCCAGGC 1980
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                                                                                                                                                                                                                                                                                                                              ValLeuProTyrValPro-----ValAlaProAspAlaGlyAsp-ArgPheAspTyrAs
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                                                                                                                                     nProTyrProGlyGlyTyrGlySerSerGly-
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Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
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R;Duncan, R.; Bazar, L.; Michelotti, G.; Tomonaga, T.; Krutzsch, H.; Avigan, M.; Levens Genes Dev. 8, 465-480, 1994
A;Title: A sequence-specific, single-strand binding protein activates the far upstream A;Reference number: A53184; MUID:94170991; PMID:8125259
A;Accession: A53184
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A53184

N;Alternate names: FUSE-binding protein - human
N;Alternate names: FUSE-binding protein
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A53184

Victoriate: 06-Jan-1995 #equence_revision 06-Jan-1995 #text_change 05-Nov-1999
C;Accession: A53184
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A;Residues: 1-644 <DUN
A;Cross-references: GB:U05040; NID:g460151; PIDN:AAA17976.1;
C;Keywords: DNA binding
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hypothetical protein ZK418.9 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t. C; Accession: T27855
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A; Residues: 1-768 < FUL>
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A;Introns: 63/2; 97/3; 121/1; 160/1; 269/3; 411/3;
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A;Residues: 1-680 <SCH's
A;Cross-references: EMBL:U88174; PIDN:AAB42272.1; GSPDB:GN00019; CESP:M01A10.1
A;Experimental Bource: strain Bristol N2; clone M01A10
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LeuAlaSerThrAlaSerProGlnGlnValSerProProAlaAlaProSerThrThrSer TCATCTTTGCAGGATTTGAGCATATACAACCCGGAAAGAACCATCACTGTGAAGGGCACA AlaAsnThrProArgLysLeuArgLeuLeuIleAlaHisSerLeuMetGlySerIleIle  ${\tt ArgGlyAlaGlyThrValPheTyrAsnProValSerArgLeuThrGlnProLeuProSer}$ GTTGAGGCCTGTGCCAGTGCTGAGATAGAGATTATGAAGAAGCTGCGTGAGGCCTTTGAA Ser-----LysAspMetLeuProGlnSerThrGluArgThrValGluIleHisGlyThr GlyArgAsnGlyLeuArgIleLysLeuIleGlnAspLysCysSerCysArgMetIleAla 214 GGAAAAGAAGGCAGAAATTTGAAGAAAATTGAACATGAAACAGGGACCAAGATAACAATC AsnValHisAspArgValLeuThrIleSerGlyProLeuGluAsnValValArgAlaTyr 154 ATAAAGAACATCACTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAACTCT ValAspAsnLeuHisAlaAlaIleTrpGluIleGlyLysCysLeuIleAspAspTrpGlu GAAGAGATTCCT-----ArgPheIleIleAspIlePheAlaLysAsnSerThrAsnProAspGlyThrProSerAsp 174 CGCATGATTCTTGAAATCATGCAGAAAGAGGCA-----ValAlaGluLeuArgSerThrThrAsnValLysAlaGlyVal---ThrLysAlaValPro GGAGCTGCAGAGAAGCCTGTCACCATCCATGCCACCCCAGAGGGGACTTCTGAAGCATGC CTGCGGATCCTGGTCCCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACC ThrGlyIleAlaLysValSerIleProThrProLysProSerThrProLeuSerThrLeu  ${\tt GluAsnSerPhePheAspValThrPheGlnAspGluProAspGluThrThrSerThrAla}$ LeuArgAlaLeuLeuSerThrArgGluAlaGlyIleIleIleGlyLysAlaGlyLysAsn  ${\tt ProProIleSerAlaLysProProMetAspAspAlaThrTyrAlaThrGlnGlnLeuThr}$ AGACAGATT ThrAsnGlySerThrIleGlnGlnSerMetThrAsnGlnProGluProThrSerGlnVal CAGCGTGGGGACCACTCTTCCCGGGAGCAAGGCCACGCCCCTGGGGGGCACTTCTCAGGCC -CTGAAAATCTTGGCACACAATGGCTTGGTTGGAAGACTGATT AATGATATGCTGGCTGTTAACACCCACTCC ---CCTTCGCCCCCT---CAGCGAGCC -GATGAGACCAAACTAGCC -GATTTCCCG 272 1119 1149 1059 1119 232 252 194 834 134 774 714 95 576 654 75 636 55 35 555

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probable RNA-binding protein - Arabidopsis thaliana
N;Alternate names: protein T32M21.30
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: T48439
R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24487
A;Accession: T48439
A;Accession: T48439
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A; Note: T32M21.30
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A;Experimental source: cultivar Columbia; BAC clone T32M21
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A; Residues: 1-313 <BEV>
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                                          {\tt IleThrGluPheGlnAlaLysSerGlyAlaArgIleGlnLeuSerArgAsnGlnGluPhe}
                                                                                           ATAAAGAACATCACTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAAC---
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C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: O2-Mar-2001 #sequence_revision O2-Mar-2001 #text_change 31-Dec-2001
C.Accession: C86275
R.Fineologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Comm, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Chin, C.W.; Chung, M.K.; Comn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
Nature 408, 816-820, 2000
Nature 408, 11, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Khaykin, E.; Kim, C.
A.; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Roomey, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Roomey, T.; Rowley, D.; Sakano, H.
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C;Genetics:
                                                                                                                              A; Molecule type: DNA
A; Residues: 1-479 <STO>
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Qy 1159 TCCAGCCTGTACCCCCATCACCACTTTGGCCCGTTCCG 1197 Db 233 SerSerSerSerMetHisGlnProGLyAlaMetLeuMetSerAlaAlaLeuThrSer 252 Qy 1158 CATCATCACTCTTAT	2 11 10	Pred. No.:   4.19e-08
US-09-270-437D-8 (1-3283) x S46109 (1-413)  QY 523 ATTTCCTACATCCCGGATGAAGAGGTGAGCTCCCCTTCGCCCTCAGCGAGCCCAGCGT 582	Alignment Scores:  Pred. No.:  8.87e-08  Matches:  Percent Similarity:  42.20%  Best Local Similarity:  24.08%  Query Match:  3.90%  Gaps:  Alignment Scores:  413  Conservative:  79  Matches:  179  Matches:  179  Gaps:  19	Dy 1354 AGGGMANGGATGGTCATCACCAGGGGCCACCGGAA.  Discrete Company of the Company of

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                                                                                  LeuThrileArgGlyThrPheMetAlaSerGlnAlaAlaIleMetLeuIleSerAsnLys
                                                                                                                                                                                                                                                                                                                                                                            AACTTCTTTAACCCCAAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCC 1497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAGGATTTGAGCATATACAACCCGGAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCC
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                                                                                                                                                                                                                                                                                        IlePheIleAspGluLys-----
                                                                                                                                                                                                                                                                                                                                                                                                                      GlyProVallleSerProAlaProGlyAsnHisLeuLeuMetAsnPheValGlnGlnGlu 334
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                                         ATCAGGGAAATTGTACAACAGGTGAAGCAGCAGGAGCAGAAATACCCT
                                                                                                                       GTCAGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCA---
                                                                                                                                                                  GlyCysSerIleIleIle-----GlnAspProValGluGlySerSerGluArgArg
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-GlulleAspArgSerAsnAlaGluArgLysArgArgSerPro
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A; Residues: 1-298, 'H' <AAS>
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A; Residues: 1-204,'V',206-356 <LEF>
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C;Keywords: RNA binding
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alpha-complex protein 1 - human
N;Alternate names: nucleic acid-binding protein; protein PCBP-1
C;Bpccies: Homo sapiens (man)
C;Date: 15-Feb-1996 #sequence revision 01-Mar-1996 #text_change 01-Dec-2000
C;Accession: S58529; S58523; S65678; S43489; S41378; S42472
C;Atcession: N; Wang, X; Liebhaber, S.A.
EMBO J. 14, 4357-4364, 1995
A;Title: Identification of two KH domain proteins in the alpha-globin mRNP stability com;
A;Reference number: S58523; MUID:96016208; PMID:7556077
A;Accession: S58523; MUID:96016208; PMID:7556077
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A;Molecule type: protein
A;Residues: 125-139,251-265;315-323 <KI2>
A;Residues: 125-139,251-265;315-323 <KI2>
B;Leffers, H.; Dejgaard, K.; Celis, J.E.
Bur. J. Biochem. 230, 447-453, 1995
Bur. J. Biochem. 230, 447-453, 1995
A;Title: Characterisation of two major cellular poly(rC)-binding human proteins, each co
A;Reference number: 865678; MUID:95331278; PMID:7607214
A;Accession: 865678
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A;Title: Tissue specific expression and cDNA structure of a human A;Reference number: $43489; MUID:94203810; PMID:8152927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X78137; NID:g460770; PIDN:CAA55016.1; PI A;Experimental source: AMA cells (transformed human amnion cells) A;Note: submitted to the EMBL Data Library, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                   679 TTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAGAACATCACTAAGCAGACC
                                                                                                                                                                                                                                                                                                                                  24 GluvalGlySerileileGlyLysLysGlyGluSerValLysArgIleArgGluGluSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GlyValThrGluSerGlyLeuAsnValThrLeuThrIleArgLeuLeuMetHisGlyLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGTCCCGGGTAGATATCCATAGAAAAGAGAACTCTGGAGCTGCAGAGAAGCCTGTCACC
                                                  :::
LeuThrGlyProThrAsnAlaIlePheLysAlaPheAlaMetIleIleAspLysLeuGlu 80
                                                                                                                       ATCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGCATGATTCTTGAAATCATGCAG 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NID: g444020; PIDN: CAA82631.1; PID: g444021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative: Mismatches: Indels:
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-GCCGAAGAGATTCCTÇTG 900
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                                                                                                                                                                                                              60
                                                                                                                                                                                                                                                                                                                                                        43
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RESULT 14 T04533 Typothetical protein F28J12.30 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 14-May-1999 C;Accession: T04533 R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, February 1998 A;Reference number: Z15377 A;Accession: T04533 A;Molecule type: DNA A;Residues: 1-846 <bevy 140="" 161="" 191="" 1;="" 232="" 262="" 287="" 293="" 300="" 3;="" 4="" 503="" 675="" 7="" 94="" a;cross-references:="" a;experimental="" a;introns:="" a;map="" a;note:="" bac="" c;genetics:="" clone="" columbia;="" cultivar="" embl:al021710="" f28j12="" f28j12.30<="" position:="" source:="" th=""><th>Db 1396 TTCAAGGCCCAGACGGAACGTCATCATCACCGGGCCACCGGAAGCCCAG 1395  Qy 1396 TTCAAGGCCCAGGGACCGAACCGAAACTGATCACCGGGCCACCGGAAGCCCAG 1395  Qy 1396 TTCAAGGCCCAGGGACCGATCTTTCGGAAACTGAAAGAGAA 1437  Db 337 SerLeuAlaGlnTyrLeuIleAsnAlaArgJeuSerSerGlu 350</th><th>279 1279 299</th><th></th><th>139 ProAsnSerThrGluArgAlailethr  1081 GAGATAGAGATT</th><th>Bb 81 GluaspileasnSerSerMetThrAsnSerThrAlaAlaSerArgProProValThrLeu 100  Qy 901 AAAATCTTGGCACACAATGGCTTGGTTGGAAAAGAAAGAA</th></bevy>	Db 1396 TTCAAGGCCCAGACGGAACGTCATCATCACCGGGCCACCGGAAGCCCAG 1395  Qy 1396 TTCAAGGCCCAGGGACCGAACCGAAACTGATCACCGGGCCACCGGAAGCCCAG 1395  Qy 1396 TTCAAGGCCCAGGGACCGATCTTTCGGAAACTGAAAGAGAA 1437  Db 337 SerLeuAlaGlnTyrLeuIleAsnAlaArgJeuSerSerGlu 350	279 1279 299		139 ProAsnSerThrGluArgAlailethr  1081 GAGATAGAGATT	Bb 81 GluaspileasnSerSerMetThrAsnSerThrAlaAlaSerArgProProValThrLeu 100  Qy 901 AAAATCTTGGCACACAATGGCTTGGTTGGAAAAGAAAGAA
Qy       928	Qy 838 ATGATTCTTGAAATCATGCAGAAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCT 897    1	Qy 718 AAGAACATCACTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAACTCTGGA 777	565 315 625 328 658 658	Db 268 LeuLeuAspSerTyrGlyHisThrIleGlyValAsnThrAlaThrPheThr 284  Qy 418	Alignment Scores:  2.62e-07  Pred. No.:  2.62e-07  Alignment Scores:  2.4.00  Matches:  117  Percent Similarity:  3.61%  Best Local Similarity:  19.28%  Query Match:  2.5  DB:  US-09-270-437D-8 (1-3283) x T04533 (1-846)  Qy  370 CTTTTGGCTCAATATGGGACAGGTGGAACAAGTCAACACA

RESULT 15 A44125 A44125 A14125 A14125 A14125 A14125 A14126 A14126 A14126 A14127 C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Accession: A44125 C;Accession: A44125 R;McKnight, G;L; Reasoner, J; Gilbert, T; Sundquist, K.O.; Hokland, B; McKernan, P.A J. Biol. Chem. 267, 12131-12141, 1992 A;Title: Cloning and expression of a cellular high density lipoprotein-binding protein tallocession: A44125; MUID:92291094; PMID:1318310 A;Accession: A44125 A;Status: preliminary	1762 800		755 1642	QY 1522 GGTGGCAAAGACCGTGAACGAACTGCAGAACTTAACCAGTGCAGAAGTCATCGTGCCTCGT 1581	Db 695 LysSerMetAlaValGuAlaValLeuLeuGLDGluTyrlleAsnAspGluAspAla /14  Qy 1462 GTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCCACAGCTGGCCGGTGATTGGCAAA 1521  ;;;;	675 GluIleLeuPheCysCysLeuSerThrProPheValPheMetGlnSerProAspAspMet  1420	Qy 1327 ATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTCATCATCACCGGGCCACCG 1386 :::          Db 655 ValasnaspSerArgThrLysCysGlyAspAspGluCysVallleIleValThrAlaThr 674 Oy 1387 GAAGCCCAGTTCAAGGCCCAGGGACGGATCTTT	1267 ATCGGGAAGAAGGGGCACACATCAAACAGCTGGCGAGATTCGCCGGAGCCTCTATCAAG	Qy 1156	1114 559 ThrGlyPhe 1123GATATG ::: 579 PheAsnAla	1066 GCCTGTGCCAGTGCTGAGATAGAGATTATGAAGAAGCTGCGTGAGGCC
Db 619 AlaGluAsnSerAsnSerGluThrIleIleIleIIeThrGlyLysArgAlaAsnCysGluAla 638  Qy 1069 TGTGCCAGTGCTGAGATAGAGATTATGAAGAAGCTGCGTGAGGCCTTTGAAAATGATATG 1128		901 589			Qy 661 ATCCTGGTCCCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAG 720	Ob 475 Sergiulysserasnieulieargirearusiyasp	455 GlyAlaAsnIleAs 571 CGAGCCCAGCGTGG		-09-270-437D-8 (1-3283) x A44125 (1-1268)  460 GAAGAAGCAAAAATAGCCATGGAGAAGCTAAGCGGG	Alignment Scores:  Pred. No.:  \$23.00	A; Molecule type: mRNA A; Residues: 1-1268 < MCK> A; Residues: 1-1268 < MCK> A; Cross-references: GB:M64098; GB:M83789; NID:g183891; PIDN:AAA35962.1; PID:g18389 A; Note: sequence extracted from NCBI backbone (NCBIN:106862, NCBIP:106863) C; Superfamily: vigilin

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BB.M64098; GB.M83789; NID:g183891; PIDN:AAA35962.1; PID:g183892
racted from NCBI backbone (NCBIN:106862, NCBIP:106863)
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|snileAsnArgileLysAspGlnTyrLysValSerValArgileProProAsp 474
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FITAACACCCACTCCGGATACTTCTCCAGCCTGTACCCCCATCACCAGTTTGGC 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  serAspIleValGlnLeuArgGlyProLysAsnGluValGluLysCysThrLys 568
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.ysArgGluLeuLeuGluLeuAlaSerArgMetGluAsnGluArgThrLysAsp 511
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ys-----SerAsnLeuIleArgIleGluGlyAsp---ProGlnGlyValGln 491
                                                                                             SerArgIleLeuSerIleGlnLysAspLeuAlaAsnIleAlaGlu------
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                                                                                                                                                                                                                                                                                    kshSerAsnSerGluThrIleIleIleThrGlyLysArgAlaAsnCysGluAla 638
                                                                                                                                                                                                                                                                                                                                                                        ACCCG---GAAAGAACCATCACTGTGAAGGGC-----ACAGTTGAGGCC 1068
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40 A0	Db 99	DD QQ	Db Qy	Db Qy	Qу	dg Qy	Db Qy	DЬ
1669 792	1609 773	1549 755	1489 735	1429 720	1369 701	1309	1249 663	656
GAAATTGTACAACAGGTG 1686 :::::    :: AlaLeuIleGlnAsnLeu 797	GTGATCGTCAGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCACAGGGCAAGATCAGG 1668 ::::::           :::            LeuIleThrIleIleGlyLysGluAspAlaValArgGluAlaGlnLysGluLeuGlu 791	AACTTAACCAGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAA 1608 :::	CCCTCTTCCACAGCTGGCCGGGTGATTGGCAAAGGTGGCAAGACCGTGAACGAAC	AAAGAGGAAAACTTCTTTAACCCCAAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTG 1488             :: AlaGluGluLysGlnThrLysSerPheThrValAspIleArgAla 734	ATCATCACCGGGCCACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAACTG 1428	GCCGGAGCCTCTATCAAGATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTC 1368 	CAGGCTGTGGGCGCCATCATCGGGAAGAAGGGGGGCACACATCAAACAGCTGGCGAGATTC 1308 ::: ::::::                       ::::::::	:::        ValGluValSerIleProAla 662

Search completed: July 23, 2004, 11:18:18 Job time: 80.5997 secs

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Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09270437/runat_23072004_095739_27413/app_query.fasta_1.5582
-DB=SwissProt_42 - QFMT=fastan - SUPFIX=rsp -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-UCTEMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09270437_@CGN 1 1 57 @runat 23072004 095739 27413 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XCAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Q92945 homo sapien
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	ALIGNMENTS	PCB2 HUMAN NOA1 MOUSE NOA1 MOUSE NOA1 HUMAN VGLN CHUMAN VGLN CHUMAN VGLN CHUMAN PAB2 ARATH S160 YEAST ROK HUMAN ROK RABIT YHLI EBV YBD2 YEAST PCLO HUMAN AFC RAT NR54 HUMAN AFC RAT NR54 HUMAN AFC RAT NR54 HUMAN AFC RAT NR54 HUMAN AFC RAT NR54 HUMAN AFC RAT NR54 HUMAN AFC RAT NR54 HUMAN AFC RAT NGUSE MILL2 HUMAN PABP SCHPO ATX7 HUMAN PABP SCHPO ATX7 MOUSE MINT HUMAN YBB7 BACTN YBB7 BACTN NGTB MOUSE YAV2 XANCV
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-!- FUNCTION: May interact with single-stranded DNA from the far-
upstream element (FUSE). May activate gene expression.
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- ALTERNATIVE PRODUCTS:
-!- ALTERNATIVE PRODUCTS:
-!- SYENT-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                               CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50084; KH TYPE 1; 4.
Transcription regulation; Trans-acting factor; Nuclear protein; DNA-binding; Repeat; Alternative splicing.
DOMAIN 77 141 KH 1.
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EMBL; BC007874; AAH07874.1; -.
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InterPro; IPR004088; KH_type_1.
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Note=No experimental confirmation available;
TISSUE SPECIFICITY: Detected in a number of cell lines.
SIMILARITY: Contains 4 KH domains.
CAUTION: Ref.1 sequence differs from that shown due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   frameshift in position 18.
CAUTION: Ref. 2 (AAH01325) sequence differs from that shown a frameshift in position 527.
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                            IsoId=Q96I24-1; Sequence=Displayed
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                                                        pAspGlyValGlyAsnGlnLeuGlyAlaLeuValHisGlnArgThrValIleThrGlu--
                                                                                    CCTTCGCCCCCTCAGCGAGCCCAGCGTG----
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                                                GTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTGATCGTCAGAATTATCGGGCAC 1632
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between
                                                                                                                                                                          Pfam; PF00013; KH; SMART; SM00322; KH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Neurochem. 82:1039-1046(2002).

-!- FUNCTION: Part of a ternary complex that binds to the downstre control sequence (DCS) of the pre-mRNA. Mediates exon inclusic transcripts that are subject to tissue-specific alternative splicing. May interact with single-stranded DNA from the farupstream element (FUSE). May activate gene expression (By similarity). Binds to the dendritic targeting element and may
                                                                                                                                               PROSITE; PS50084; KH_TYPE_1;
                                                                                                                                                                                                                               InterPro; IPR004087;
InterPro; IPR004088;
                                                                                                                                                                                                                                                     EMBL; AF308818; AAG59811.1; -. InterPro; IPR004087; KH_dom.
                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a role in mRNA trafficking.

-!- SUBUNIT: Part of a ternary complex containing FUBP2, and HNRPH1 (By similarity).

-!- SUBCELLULAR LOCATION: Nuclear. A small proportion is the cytoplasm of neuronal cell bodies and dendrites.

-!- SIMILARITY: Contains 4 KH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rehbein M., Wege K., Buck F., Schweizer M., Richt "Molecular characterization of MARTA1, a protein dendritic targeting element of MAP2 mRNAs.";
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Far upstream element binding protein 2 (FUSE binding protein 2)
type splicing regulatory protein) (KSRP) (MAP2 RNA trans-acting
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Mammalia; Eutheria; Rodentia;
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-AGTGAGGCTCCCACAGGCACCAGCAAAACAACGGATGAATGTAGCCCTT
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RX MEDLINE-22386257; PubMed=12477932;

RA Altausherg R.D., Collins F.S., Wagner L.H., Derge J.G.,

RX Klausher R.D., Collins F.S., Wagner L. Shenmen C.M., Schuler G.D.,

RX Klausher R.D., Collins F.S., Wagner L. Shenmen C.M., Schuler G.D.,

RX Klausher R.D., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

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RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RX Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RX Hopkins R.F., Jordan H., Fobraid M.F., Cassavant T.L., Scheetz T.E.,

RX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RX Raha S.S., Mocen P.J., McKernan K.J., Abramson R.D., Mullahy S.W.,

RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Rahellon D.K., Morra M., Gay L.J., Hulyk S.W.,

RX Richards S., Worley K.C., Hale S., Garcia A.M.,

RX Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RX Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RX Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RX Rodriguez A.C., Grimwood J., Schmutz J., Myers R
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
Far upstream element binding protein 1 (FUSE
(DNA helicase V) (HDH V).
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Duncan R., Bazar L., Michelotti G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
                                                                                                             SEQUENCE OF 45-64; 133-145; 271-283; 308-321; 379-386;
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   Vindigni A., Ochem
                                     MEDLINE=21127960; PubMed=11222755;
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           Triolo G.,
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                                                                                                                                                                                            99:16899-16903 (2002)
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                  Falaschi A.;
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                              PROSITE; PS50084; KH TYPE 1;
Transcription regulation; Tr
DNA-binding; Repeat; Ubl con
                                                                                                                              EMBL; U05040; AAA17976.2; -.
EMBL; BC017247; AAH17247.1;
PDB; 1J4W; 06-MAR-02.
                                                                      InterPro; IPR004088; Pfam; PF00013; KH; 4.
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                     3D-structure.
                                                             SMART; SM00322; KH;
                                                                             InterPro; IPR008160; Collagen.
InterPro; IPR004087; KH_dom.
InterPro; IPR004088; KH_type_1.
                                                                                                              MIM; 603444;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21864720; PubMed=11875576;
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Kim M.J., Park B.-J., Kang Y.-S.,
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He L., Collins
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PTM: Ubiquitinated, This
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                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=2;
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                                                                                                                       HGNC:4004; FUBP1.
                                                                                                                                                                                                                                                                                              IsoId=Q96AE4-2;
                                                                                                                                                                      s requires a license agreement (Some an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                      Sequence=VSP_008321;
ental confirmation available;
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                                                               GGAAAGAACC----
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RA Strausberg R.D., Collins F.S., Wagner L., Schemen C.M., Schuler G.D., RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Brownstein M.J., McKernan K.J., Malek J.A., Gunzratne P.H., RA Richards S., McDuey K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., RA Hiskesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Biakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Biakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Biakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; Figeneration and mouse cDNA sequences.", proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., RA Nagai K., Tomaru Y., Hasegawa Y., Nogami A., Goobobri T., RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., RA Balke J.A., Hill D.P., Bult C., Hume D.A., Quackenbush J., RA Balke J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., RA Balke J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., RA Balke J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., RA Balke J.A., Kanapain A., Kawasawa Y., Kedzierski R.M., King B.L., RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., RA Nagashima T., Numata K., Okido T., Bavan W.J., Pertea G., Pesole G., RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ramachandran S., RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., RA Hara A., Yashizaki Y.:
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MEDLINE=22388257; PubMed=12477932;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-OCT-2003 (Rel. 42, Last annotation update)
Far upstream element binding protein 1 (FUSE binding protein 1)
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                                                                                                                                                                                                                                                                                                                                      Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome based on functional 60,770 full-length cDNAs.";
Nature 420:563-573(2002)
                                                                             both as activator and repressor of transcription SUBUNIT: Interacts with SIAHBP1/FIR and JTV1 (By SUBCELLULAR LOCATION: Nuclear (Probable).
                                                                                                                                                                                               FUNCTION: Regulates MYC expression by binding to a single-stranded far-upstream element (FUSE) upstream of the MYC promoter. May act both as activator and repressor of transcription (By similarity)
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splicing; Named isoforms=2;
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Sciurognathi; Muridae; Murinae; Mus
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, Kiyosawa H.,
C., Gojobori T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  annotation
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DB:
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                No.:
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MGD; MGI:1924642; 9530027K12Rik.
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                                                                                                                                                                                                                                   GAATGTGGAACAAGTCAACACAGACACAGAAACCGCCGTTGTCAACGTCACATAT-----
                                                                                                    uAsnSerAsnAspTyrGlyTyrGlyGlyGlnLysArgProLeuGluAspGlyAspGlnPr
                                                                                                                              TCAGTTTGAGAACTACTCCTTCAAGATTTCCTACATCCCGGATGAAGAGGTGAGCTCCCC
                                                                                                                                                       pAlaLeuGlnArgAlaArgGlnIleAlaAlaLysIleGlyGlyAspAlaGlyThrSerLe
                                                                                                                                                                                                                                                                                     CCCTCCTCACCTGCAGTGGGAGGTGTTGGATGGACTTTTGGCTCAATATGGGACAGTGGA 395
                         oAspAlaLysLysValProProGlnAsnAspSerPheGlyAlaGlnLeu
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651 AA;
-ProProMetHisGlnGlnGlnSerArgSerVal---MetThrGluGluTyrLy
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68539
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MISSING (IN REF. 2).
F4EECA62FD9FA0D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
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     {\tt rIleSerGlnGlnSerGlyAlaArgIleGluLeuGlnArgSerProProProAsnAlaAs}
                               ACTGCAGAACTTAACCAGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAA 160
                                                                      CAGAGTGCCCTCTTCCACAGCTGGCCGGGTGATTGGCAAAGGTGGCAAAGACCGTGAACGA
                                                                                                                                                            oGlyProGlyGlyArgGlyArgGlyGlnGlyAsnTrpAsnMetGlyProProGl
                                                         ----ValProThrGlyLysThrGlyLeuIleIleGlyLysGlyGlyGluThrIleLysSe
                                                                                                              yGlyLeuGlnGluPheAsnPheIle--
                                                                                                                                     ----CTGAAAGAGGAAAACTTCTTTAACCCCAAAGAAGAAGTGAAGCTGGAAGCGCATAT
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Q92945; 000301; Q9UNTS; Q9UQHS;

10-CCT-2003 (Rel. 42, Created)

10-CCT-2003 (Rel. 42, Last sequence update)

10-CCT-2003 (Rel. 42, Last annotation update)

Far upstream element binding protein 2 (FUSE binding protein type splicing regulatory protein) (KSRP) (p75).
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"A new regulatory protein, KSRP, mediates exon intronic splicing enhancer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., SEQUENCE OF 72-85; 123-128; 348-359; 472-486; 488-492; 620-625; 627-644 AND TISSUE-Neuroblastoma, and Retinoblastoma; MEDLINE-97282621; PubMed-9136930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                        "The far upstream element-binding proteins comprise an of single-strand DNA-binding transactivators.";
J. Biol. Chem. 271:31679-31687(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mapping of the KHSRP gene to a region of conserved chromosome 19p13.3 and mouse chromosome 17."; genomics 56:350-352(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-115 AND 570-707 FROM N.A. MEDLINE=99189245; PubMed=10087204; Ring H.Z., Vameghi-Meyers V., Nikolic J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
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                                          Markovtsov V., Black D.L.;
                                                                            MEDLINE=20459250; Pubme
                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=B-cell lymphoma, and Skele MEDLINE=97094955; PubMed=8940189;
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assembly of an hnRNP complex induced by
                                                                                                                                                                 INTERACTION WITH PTBP1;
                                                                                                                           PubMed=11003644;
                                                                                         J.M.,
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                                                                                         Goldman J.A., Turck C.W.,
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US-09-270-437D-8

 $(1-3283) \times FUB2_HUMAN$ 

(1-707)

104 CCGCCGTCACCGCCGACGACCTCCGGCAGCTCTTTGGGGACAGGAAGCTGCCCCTGGCGG

proproGlyproProProProAlaGlyGlyGlyGlyAlaGly-GlyAlaGlyGlyGl

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Query
DB:
         Best Local Similarity:
Query Match:
                                    Percent Similarity:
                                                                       Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue-specific homolog of polypyrimidine tract binding protein.";
Mol. Cell. Biol. 20:7463-7479(2000).

-I- FUNCTION: Binds to the dendritic targeting element and may play a role in mRNA trafficking (By similarity). Part of a ternary complex that binds to the downstream control sequence (DCS) of the pre-mRNA. Mediates exon inclusion in transcripts that are subject to tissue-specific alternative splicing. May interact with single-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF093747; AAD29861.1; -.
EMBL; AF093745; AAD29861.1; JOINED.
EMBL; AF093740; AAD29862.1; -.
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CONFLICT
CONFLICT
CONFLICT
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REPEAT
DOMAIN
                                                                                                                                                                                                                                                                                                                                                SMART; SM00322; KH;
                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00013; KH; 4.
                                                                                                                                                                                                                                                                                                                                                                                               MIM; 603445; -
                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:6316; KHSRP.
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U69126; AAC50892.1; ALT_FRAME
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                                                                                                                                                                                                                                                                                                   DNA-binding;
                                                                                                                                                                                                                                                                                                              Transcription regulation;
                                                                                                                                                                                                                                                                                                                           Transport; mRNA transport;
                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR004088; KH_type_1.
                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                  REPEAT
                                                             No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and HNRPH1.
SUBCELLULAR LOCATION: Nuclear.
the cytoplasm of neuronal cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
TISSUE SPECIFICITY: Detected in neural and non-neural SIMILARITY: Contains 4 KH domains.
CAUTION: Ref.3 sequence differs from that shown due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene expression. SUBUNIT: Part of a ternary complex containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stranded DNA from the far-upstream element (FUSE). May activate
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                                                                                                                                                                                                                                                                                                                                     PS50084; KH_TYPE_1; 4
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233
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422
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641
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                                                                                                                                                                                                                                                                                                   RNA-binding; Repeat.
            4.42e-09
259.00
33.38%
20.99%
4.40%
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                                                                                                 707
72709
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                                                                                                                                                                                                                                                                                                                 Trans-acting
                                                                                                                                                                                                                                                                                                                             mRNA
                                                                                                                                 GLY/PRO-RICH.
GLY-RICH.
ALA/GLY/PRO-RICH.
G-> V (IN REF. 2).
V -> G (IN REF. 2).
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                                                                                                 -> GG (IN REF. 2)
-> A (IN REF. 2)
E07588DE43BCA8B6
                                                                                                                                                                                                                                                                                                                 processing; mRNA splicing;
-acting factor; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A small proportion is bodies and dendrites (
                                                 Length:
Matches:
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                                                                                                                        2).
                                                                                                   CRC64;
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$\omega + \omega +$	947 AAGGCAGAAATTTGAAGAAAATTGAACATGAAACAGGGACGAAGATAACAATCT 1000	862	746 GGGTAGATATCCATAGAAAAGAAACTCTGGAGCTGCAGAGAAAGCCTGTCACCATCCAT	626 CTTCTCAGGCCAGACAGATTGATTTCCCGCTGCGGATCCTGGTCCCCACCCA	512 ACTCCTTCAAGATTTCCTACATCCCGGATGAAGAGGTGAGCTCCCCTTCGCCCCCTCAGC 571 ::	398 ATGTGGAACAAGTCAACACAGACACAGAAACCGCCGTTGTCAACGTCACATATGCAACAA 457  80 rgAlaArgGlnile	ATTACTCAGTCTCTAAAAAGCTAAGGAGAGGAAAAATTCAGAATTCCGAAACATCCCTCCTC	164 GACAGGTCCTGCTGAAGTCCGGCTACGCCTTCGTGGACTACCCCGACCAGAACTGGGCCA 223
Qy 1954 CGAGCCCGCCTCCGGCCCCCAG 1977	QY 1843 CCATCTGAGGAATGAGAAGTCTGCGGAGGCGCCAGGGATCTGCCGAGGC 1893  Db 572 laAlaTrpAlaAlaTyrTyrSerHisTyrTyrGlnGlnDroProGlyProValPro 590  QY 1894 CCTGAGAACCCCAGGGGCGGGAGGGGGGGGAAGGTCAGGTCTGCCAGAACCAC 1953	1777 RAGCUCTTCAACACCTGA	1661 492 1717 512	1562 CAGAAGTCATCGTGCC	1442 418 1502 434	378 rgCys 1420 398 roGly	GAGATTCGCCGGAGCCTCTATCAAGATTGCCC	Oy 1181 AGTTTGGC

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MEDLINE-21640447; PubMed-11781334;
Gu W., Pan F., Zhang H., Bassell G.J., Singer R.H.;
"A predominantly nuclear protein affecting cytoplasmic localization beta-actin mRNA in fibroblasts and neurons.";
J. Cell Biol. 156:41-52 (2002).
-i- FUNCTION: Binds to a 54-nucleofide localization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Archosauria; Aves; Neognathae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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10-OCT-2003
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GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:0003730; F:mRNA 3' UTR binding; IDA.
GO; GO:0003730; F:mRNA localization, intrac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00013; KH; 4. SMART; SM00322; KH; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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InterPro; IPR004088; KH_type_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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FUNCTION: Binds to a 54-nucleotide localization signal (the FUNCTION: Binds to a 54-nucleotide region of beta-actin mRI zipcode) found in the 3' untranslated region of beta-actin mRI and may play a role in its localization.

SUBCELLULAR LOCATION: Predominantly nuclear. Also detected in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \bar{\text{DEVELOPMENTAL}} STAGE: The highest expression is embryos, is reduced to 30% before hatching and thereafter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 4 KH domains.
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182
                                                           132
                                                                                                                                                                                                                                                    160 ArgSerGlyProValGlyAspProProGlyProProArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS50084;
                                                        GCTCTTTGGGGACAGGAAGCTGCCCCTGGCGGACAGGTCCTGCTGAAGTCCGGCTACGC
                                                                                                                                                                                         GATGAACAAGCTTTACATCGGGAACCTGAGCCCCGCCGTCACCGCCGACGACCTCCGGCA
                                                                                                                                                                                                                                                                                                             аросси в предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоставления предоста
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(Rel. 42, Last annotation
ling protein 2.
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transport; Nu
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259.00
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Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80644 MW;
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Nuclear protein;
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4.3.
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   -ThrGlyGlyAlaLeuProSer-
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Matches:
Conservative:
Mismatches:
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RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F., Ra Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E., Ra Braeken M., Weltjens I., Voet M., Hilbert H., Braun M., Ra Holzer E., Brandt A., Peters S., van Staveren M., Dirkee W., Ra Holzer E., Brandt A., Peters S., van Staveren M., Dirkee W., Ra Holzer E., Brandt A., Peters S., van Staveren M., Dirkee W., Roeiman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., Ra Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., Ra Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., Ra Mooijman P., Klein Lankhorst R., Vallarroel R., De Clercg R., Vallarroel R., De Clercg R., Ray M., Lennard N., Mayes R., Petert A., Rojandream M.A., Lyne M., Benes V., Rechmann S., Petert A., Rajandream M.A., Lyne M., Benes V., Rechmann S., Ray M., Loehnert T.-H., Dose S., de Haan M., Maarse A., Schaefer M., Mueller-Auer S., Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H., Dose S., de Haan M., Maarse A., Schaefer M., Mueller-Auer S., Babel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A., Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R., Schmidt W., Lecharny A., Aubourg S., Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E., Casacuberta E., Casacuberta E., Schmidt W., Lecharny A., Aubourg S., Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E., Casacuberta E., Schmidt M., Berger C., Monfort A., Casacuberta E., Casacuberta E., Casacuberta E., Piras M., Peter P., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T., Van Peter P., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
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Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
Langham S.-A., McCullagh B., Bilham L., Robben J.,
Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
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16-OCT-2001 (Rel
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Putative nucleic acid binding protein At4g18375
AT4G18375 OR F28J12.2.
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MEDLINE=20083488; PubMed=10617198;
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M., Terol J., Torres A.,
n S., Tacon D., Jesse T.
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Hypothetical protein; Nuclear Alternative splicing.
DOMAIN 35 99 F

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Pfam; PF00013; KH; 5. SMART; SM00322; KH; 5.

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InterPro; IPR004087; KH\_dom. InterPro; IPR004088; KH\_type\_1.

PROSITE; PS50084; KH\_TYPE

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protein;

RNA-binding; Repeat;

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AR Prishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Prishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Parnell L., Dedhia N., Wilson R.K., de la Bastide M., Habermann K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Schkon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W.,
RA Nelson J., Spieth J., Ryan B., Andrews S., Geisel C., Layman D.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RS Swaby I.K., O'Shaugnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohdy N., Hasegawa A., Hameed M., Lodhi M., Johnson A.,
Chen E., Marra M.A., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
EMBL; AL021710; CAA16717.1; ALT SEQ. EMBL; AL161548; CAB78839.1; ALT SEQ. EMBL; AY133701; AAM91635.1; -. EMBL; BT001108; AAN64172.1; -.
                                                                                                                                                                                                        Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J., Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F., Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G., Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J., Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y., Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P., Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F., Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M., Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J., Xamiya A., Meyers C., Nakajima M., Narusaka M., Saki M., Sakurai T., Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y., "Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 302:842-846(2003).
-!- SUBCELLULAR LOCATION:
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome."
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MEDLINE=22954850; PubMed=14593172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  gene model prediction. At4g18370 and fused into a single gene.
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Note=May be due to a competing acceptor site. No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P58223-1;
                                                                                                                                                                      s requires a license agreement (S an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                           There
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/FTId=VSP 008900.
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                                                                                                                               SEQUENCE FROM N.A.

MEDILINE=20396135; PubMed=10936052;

Makeyev A.V., Liebhaber S.A.;

"Identification of two novel mammalian genes
of KH-domain RNA-binding proteins.";

Genomics 67:301-31(2000).
                                                                -i- FUNCTION: Single-stranded nucleic acid binding preferentially to oligo dC (By similarity).
-i- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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                              TISSUE SPECIFICITY: Ubiquitous. SIMILARITY: Contains 3 KH domains
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores: Pred. No.: Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1890470; Pcbp3.
InterPro; IPR004087; KH_dom.
InterPro; IPR004088; KH_type_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF176327; AAG
HSSP; Q07244; 1KHM.
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                                                                                                                                    1045 ACTGTGAAGGGCACAGTTGAGGCCTGTGCCAGTGCTGAGATAGAGATTATGAAGAAGCTG
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SM00322; KH; 3.
'E; PS50084; KH TYPE 1; 3.
'X protein; RNA-binding; R
rIleProTyrArgProLysProAlaCysThrProValIlePheAlaGlyGlyGlnAlaTy
                                                                               CGTGAGGCCTTTGAAAATGATATGCTGGCTGTTAACACCCACTCCGGAT------
                                                                                                                                                              AlaGlnValGlnValAlaGly-----AspMetLeuProAsnSerThrGluArgAlaVal
                                                                                                                                                                                         ACCAAGATAACAATCTCATCTTTGCAGGATTTGAGCATATACAACCCGGAAAGAACCATC
                                                                                                                                                                                                                   CysGlySerLeuileGlyLysGlyGlySerLysIleLysGluileArgGluSerThrGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTGATTTCCCGCTGCGGATCCTGGTCCCCACCCAGTTTGTTGGTGCCATCATCGGAAAG
                                                                                                                                                                                                                                                                         \tt AsnSerProAlaThrSerLysProProValThrLeuArgLeuValValProAlaSerGln
                                                                                                                                                                                                                                                                                                 GATGAGACCAAACTAGCCGAA---GAGATTCCTCTGAAAATCTTGGCACACAATGGCTTG
                                                                                                                                                                                                                                                                                                                            PheLysAlaPheAlaMetIleAlaTyrLysPheGluGluAspIleIleAsnSerMetSer
                                                                                                                                                                                                                                                                                                                                                                                                                                     LysGlyGluThrValLysLysMetArgGluGluSerGlyAlaArgIleAsnIle-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValThrLeuThrIleArgLeuLeuMetHisGlyLysGluValGlySerIleIleGlyLys
                                                                                                             ThrIleSerGlyThrProAspAla-Ile
                                                                                                                                                                                                                                               GTTGGAAGACTGATTGGAAAAGAAGGCAGAAATTTGAAGAAAATTGAACATGAAACAGGG
                                                                                                                                                                                                                                                                                                                                                          TCTGAAGCATGCCGCATGATTCTT-------GAAATCATGCAGAAAGAGGCA
                                                                                                                                                                                                                                                                                                                                                                                  ----SerGluGlyAsnCysProGluArgIleValThrIleThrGlyProThrAspAlaIle
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                  -ACTTCTCCAGCCTGTACCCCCATCAC-
                                                     LysGlnIleCysValValMetLeuGluSerProProLysGlyAlaTh
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Mismatches:
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Gaps:
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P57721;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of KH-domain RNA-binding proteins.";

Genomics 67:301-316(2000).

-I- FUNCTION: Single-stranded nucleic acid binding preferentially to oligo dC (By similarity).

-I- SUBCELLULAR LOCATION: Nuclear (By similarity).
                     InterPro; IPR004087; KH_dom.
InterPro; IPR004088; KH_type_1.
Pfam; Pf00013; KH; 3.
SMART; SM00322; KH; 3.
                                                                                                                   Genew; HGNC:8651; PCBP3.
GO; GO:0005634; C:nucleus; ISS.
GO; GO:0003677; F:DNA binding; ISS.
GO; GO:0003723; F:RNA binding; NAS.
GO; GO:0016671; P:mRNA metabolism;
                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
PROSITE;
                                                                                                                                                                                                                                                       EMBL; AF176329;
HSSP; Q07244; 11
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MEDLINE=20396135; PubMed=10936052;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Creat
16-OCT-2001 (Rel. 40, Last
16-OCT-2001 (Rel. 40, Last
Poly(rC)-binding protein 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens

    !- SIMILARITY: Contains 3 KH domains.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Identification of two novel mammalian genes establishes a
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                                                                                                                                                                                                                                                                                                                                         an email to license@isb-sib.ch).
PS50084; KH
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Edal
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annotation
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A Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsteh F.,

A Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

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A Steapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Blosak S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,

A Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,

A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length

"Thimson and more of Marka Commonce" "In Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara I Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.;
"NEDO human cDNa sequencing project.";
"NEDO human cDNa sequencing project.";
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MEDLINE=20396135; PubMed=10936052;

Makeyev A.V., Liebhaber S.A.;

"Identification of two novel mammalian
of KH-domain RNA-binding proteins.";

Genomics 67:301-316(2000).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                      -!- FUNCTION: Single-stranded nucleic acid binding preferentially to oligo dC (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                 human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                         -!- SIMILARITY: Contains 3 KH domains.
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SEQUENCE
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GO; GO:0003677; F:DNA binding; ISS.
GO; GO:0003723; F:RNA binding; NAS.
GO; GO:00160771; P:mRNA metabolism;
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EMBL; AK023993; BAB14761.1; --
EMBL; AK023908; AAH03008.1; --
EMBL; BC004153; AAH04153.1; --
Genew; HGNC.8652; PCBP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
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InterPro; IPR004088; KH_type_1.
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AsnSerThrGluArgAlaValThrValSerGlyValProAspAlaIleIleLeuCysVal
                           GACGTCAGCGAAAGGATGGTCATCATCACCGGGCCACCGGAAGCC
                                                                               ATCARACAGCTGGCGAGATTCGCCGGAGCCTCTATCAAGATTGCCCCTGCGGAAGGCCCA
                                                                                                           LeuArgLeuValileProAlaSerGlnCysGlySerLeuIleGlyLysAlaGlyThrLys
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RNA-binding; Ribonucleoprotein;
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P38151;
01-OCT-1994
 SEQUENCE FROM N.A. STRAIN=S288c;
                                                         Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                          01-OCT-1994
16-OCT-2001
                                                                                                         PAB1-binding protein 2.
PBP2 OR YBR233W OR YBR1531.
                                              NCBI_TaxID=4932;
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                                                                                                                                         (Rel. 30, Created)
(Rel. 30, Last sequence up
(Rel. 40, Last annotation
                                                                                                                                                                                                        STANDARD;
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Best Local Similarity:
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SEQUENCE
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Scherens B.,
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"Pbp1p, a factor interacting with Saccharomyces cerevisiae poly(A)
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PIR; S46109; S46109.
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SMART; SM00322; KH; 3.
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InterPro; IPR004088; KH_type_1.
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SUBCELLULAR LOCATION: Nuclear (Potential).
SIMILARITY: Contains 3 KH domains.
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      CGCATGATTCTTGAAATCATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAA----
                                     GlyValProGluArgIleValTyrValArgGlyThrCysAspAspValAlaLysAlaTyr
                                                                                                                           ATAAAGAACATCACTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAACTCT
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the EMBL/GenBank/DDBJ databases
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                          binding protein SUB2.3).
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                                                                                                                                                                                                          ATCAGGGAAATTGTACAACAGGTGAAGCAGCAGGAGCAGAAATACCCT 1710
                                                                                                                                                                                                                                                             GTCAGAATTATCGGGCACTTCTTTGCTAGCCAGACTGCA------
                                                                                                                                                                                                                                                                                                                                                                                      AACTTCTTTAACCCCAAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCC
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GO; GO:0005737; C:cytoplasm; NAS.
GO; GO:0005734; C:nucleus; NAS.
GO; GO:0005634; C:nucleus; NAS.
GO; GO:0003723; F:RNA binding; IDA.
GO; GO:0003697; F:single-stranded DNA
GO; GO:0016071; P:mRNA metabolism; NA
InterPro; IPR004087; KH_dom.
InterPro; IPR004088; KH_type_1.
InterPro; IPR004088; KH_type_1.
Pfam; PF00013; KH; 3.
SMART; SM00322; KH; 3.
PROSITE; PS50084; KH_TYPE 1; 3.
Nuclear protein; RNA_binding; Ribonuc
               DOMAIN
CONFLICT
                                                                                                                                                                                                                                                                             EMBL; X78137; CAA55016.1;
EMBL; U24223; AAA91317.1;
EMBL; Z29505; CAA82631.1;
HSSP; Q07244; IKHM.
                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 22:959-964 (1994).

-!- FUNCTION: Single-stranded nucleic acid binding protein that bind preferentially to oligo dC.
-!- SUBCELLULAR LOCATION: Loosely bound in the nucleus. May shuttle between the nucleus and the cytoplasm.
-!- TISSUE SPECIFICITY: Abundantly expressed in skeletal muscle, thymus and peripheral blood leucocytes while a lower expression observed in prostate, spleen, testis, ovary, small intestine, heart, liver, adrenal and thyroid glands.
-!- FTM: PHOSPHORYLATED. THE NON-PHOSPHORYLATED FORM(S) EXHIBITED TH STRONGEST POLY(RC)-BINDING ACTIVITY.
-!- SIMILARITY: Contains 3 KH domains.
-!- CAUTION: There is probably a frameshift error in the nucleotide
  SEQUENCE
                                           DOMAIN
                                                      Phosphorylation;
DOMAIN 13
                                                                                                                                                                                                                                       GK; Q15365; -
MIM; 601209;
                                                                                                                                                                                                                                                                  Genew; HGNC:8647;
                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                               use by non-profit institute modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aasheim H.-C., Loukianova T., Deggerdal A., Smeland "Tissue specific expression and cDNA structure of a encoding a nucleic acid binding [oligo(dC)] protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding a nucleic acid be pre-mRNA binding protein
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MEDLINE=94203810; P
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EMBO J. 14:4357-4364(1995)
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MEDLINE=95331278; PubMed=7607214;
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Mammalia; Eutheria;
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                                       GlnThrThrHisGluLeuThrIleProAsnAsnLeuIleGlyCysIleIleGlyArgGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thiele B.J., Berger M., Huth A., Reimann I., Schwarz K., "Tissue-specific translational regulation of alternative 15-lipoxygenase mRNAs differing in their 3'-untranslated Nucleic Acids Res. 27:1828-1836 (1999).

-!- FUNCTION: Single-stranded nucleic acid binding protei preferentially to oligo dC (By similarity).

-!- SUBCELLULLAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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16-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; C:
Mammalia; Eutheria; Lagomorpha;
                                                                                                                                                                                          Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ003023; CAZ
HSSP; Q07244; 1KHM.
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                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                         Nuclear protein; RNA-binding; Ribonucleoprotein; DNA-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00322; KH; 3.
                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00013; KH; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Contains 3 KH domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCGGAAGGCCCAGACGTCAGCGAAAAGGATGGTCATCATCACCGGGCCACCGGAAGCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerLeuAlaGlnTyrLeuIleAsnAlaArgLeuSerSerGlu
                                     TTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAGAACATCACTAAGCAGACC
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       GluValGlySerIleIleGlyLysLysGlyGluSerValLysArglleArgGluGluSer
                                                                                                                                                                                                                                                                                                                                                          PS50084; KH_TYPE_1; 3.
                                                                   GlyValThrGluSerGlyLeuAsnValThrLeuThrIleArgLeuLeuMetH1sGlyLys
                                                                                                                                                                                                                                                                                                                                                                                                     IPR004088; KH_type_1.
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protein 1 (Alpha-CP1) (hnR
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343 K
37497 MW;
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              TGLN HUMAN STANDARD; PRT; 1268 AA.

Q00341; Q9UCY3;

01-NOV-1997 (Rel. 35, Created)

01-NOV-1997 (Rel. 35, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)

Vigilin (High density lipoprotein-binding protein)
 protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAATCTTGGCACACAATGGCTTGGTTGGAAGACTGATTGGAAAAGAAGGCAGAAATTTG 960
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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casvant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Robask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
RA Rodriguez A.C., Shevchenko Y., Bouffard G.G.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Wyers R.M.,
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-i-FUNCTION: APPEARS TO PLAY A ROLE IT MAY FUNCTION TO PROTECT CELLS
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J. Biol. Chem. 267:12131-12141(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
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GO:0005886; C:plasma membrane; TAS. GO:0008289; F:lipid binding; TAS. GO:0008203; P:cholesterol metabolism; erPro; IPR004088; KH_Cype_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Nuclear and cytoplasmic SIMILARITY: Contains 14 KH domains.
                                                                                                                                                                                                                         A44125; A44125.
1VIG; 03-APR-96.
1VIH; 03-APR-96.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry is copyright. It is produced through iss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contains 14 KH domain STRONG, TO C.ELEGANS
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DB:
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 PheLysGlnPheHisLys-
                    AAAATCTTGGCACACAATGGCTTGGTTGGAAGACTGATTGGAAAAGAAGGCAGAAATTTG
                                                                ATTCTTGAAATCATGCAGAAAGAGGCAGATGAGACCAAACTAGCCGAAGAGATTCCTCTG
                                                                                   GlnLysSerAspIleValGlnLeuArgGlyProLysAsnGluValGluLysCysThrLys
                                                                                                           GCAGAGAAGCCTGTCACCATCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGCATG
                                                                                                                                Gluile---ArgAspLysPheProGluValIleIleAsnPheProAsp---
                                                                                                                                                      AACATCACTAAGCAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAACTCTGGAGCT
                                                                                                                                                                          LeuIleIleGluGlnArgPheHisArgThrileIleGlyGlnLysGlyGluArgIleArg
                                                                                                                                                                                                 ATCCTGGTCCCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATAAAG
                                                                                                                                                                                                                      {\tt GinAlaLysArgGluLeuLeuGluLeuAlaSerArgMetGluAsnGluArgThrLysAsp}
                                                                                                                                                                                                                                                                 SerGluLys----SerAsnLeuIleArgIleGluGlyAsp---ProGlnGlyValGln
                                                                                                                                                                                                                                                                                                             GlyAlaAsnIleAsnArgIleLysAspGlnTyrLysValSerValArgIleProProAsp
                                           TyrMetGlnLysMetValAlaAspLeuValGluAsnSerTyrSerIleSerValProIle
                                                                                                                                                                                                                                              CAGGCCAGACAG-----ATTGATTTCCCGCTGCGG------
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                                                                                                                                                                                                                                                                                                                                   TCCTTCAAGATTTCCTACATCCCGGATGAA---GAGGTGAGCTCCCCTTCGCCCCTCAG
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PHOSPHORYLATION (POTENTIAL).

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Q80WA4;
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                                                                        STRAIN=BDIX; TISSUE=Cerebellum; Knudsen A., Monstad S.E., Vedeler C.A.;
                                                                                                  SEQUENCE FROM N.A.
STRAIN-BDIX; TISSUE-Cerebellum;
                                                                                                                                                                                                                                                                                                                        RNA-binding
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                  NCBI_TaxID=10116;
                                                                                                                                                                                                 Mammalia; Eutheria;
                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                              "Nova-1, the paraneoplastic Ri antigen,
                                                                                                                                                                                                                                                                                                 (Fragment)
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(Rel. 42, Last sequence update)
(Rel. 42, Last snnotation update)
protein Nova-1 (Neuro-oncological ventral antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                    Chordata;
Rodentia;
                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus
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"Role of Nova-1 in regulating alpha2N, a novel glycine receptor splice variant, in developing spinal cord neurons.";

J. Neurobiol. 52:156-165(2002).

J. FUNCTION: Functions to regulate alternative splicing in neurons binding pre-mRNA in a sequence-specific manner to activate exor inclusion. It binds specifically to the sequence UCAUY (By similarity). Acts to regulate a novel glycine receptor alpha-2 chain splice variant (alpha-2N) in developing spinal cord.

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InterPro; IPR004087; KH_dom.
InterPro; IPR004088; KH_type_1.
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Q9y6m1 homo sapien
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Q17936 caemorhabdi
Q191xf5 arabidopsis
Q9c553 arabidopsis
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Q96ep6 homo sapien
Q7z145 caemorhabdi
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## ALIGNMENTS

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RESULT 1

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D9Y6M1

PRELIMINARY; PRT; 556 AA.

AC Q9Y6M1;

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 25, Last sequence update)

DT 01-NOV-1999 (TREMBLrel. 25, Last sannotation update)

DF 0203 (TREMBLrel. 25, Last annotation update)

DF 0203 (TREMBLrel. 25, Last annotation update)

DF 0203 (TREMBLrel. 25, Last annotation update)

DF 0204 (Trembler)

DF 0205 (Trembler)

DF 0205 (Trembler)

CO Homo sapiens (Human).

OC Homo sapiens (Human).

OC Mammalia; Entheria; Primates; Catarrhini; Hominidae; Homo.

OC MARMALIA; Entheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TAXID=9606;

RN [1]

SEQUENCE FROM N.A.

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RA Zhang J.Y., Chan E.K., Peng X.X., Tan E.M.;

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RA Zhang J.Y., Chan E.K., Peng X.X., Tan E.M.;

RA Zhang J.Y., Chan E.K., Peng X.X.,
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Alignment S Pred. No.: Score:

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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InterPro; IPR004088; KM_type_1.
InterPro; IPR004088; KM_type_1.
InterPro; IPR000504; RNA_rec_mot.
pfam; pF00013; KH; 4.
Pfam; pF00076; rrm; 2.
Pfam; pF00076; rrm; 4.
SMART; SM00322; KH; 4.
SMART; SM00360; RRM; 2.
PROSITE; PS50084; KH_TYPE_1; 4.
PROSITE; PS50102; RRM; 2.
PROSITE; PS50102; RRM; 2.
SMOUGHOUSE 556 AA; 61842 MW; IEDEFB100443DDC4
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chc
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                  Chordata;
Rodentia;
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                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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RP SEQUENCE FROM N.A.

RC STRAIN=257BL/6; TISSUE=Brain;

RC STRAIN=257BL/6; TISSUE=Brain;

RC MEDLINE=223B8257; PubMed=12477932;

RA MEDLINE=223B8257; PubMed=12477932;

RA MEDLINE=223B8257; PubMed=12477932;

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow R.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Kabin G.M., Hong L.,

RA Lischerko L., Warusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soders M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Woffer G.J., Abramson R.D., Mullahy S.J.,

RA Roha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Rahes J., Hulton E., Ketteman M., Madan A., Gay L.J., Hulyk S.W.,

RA Hahey J., Helton E., Ketteman M., Machan A., Rodrigues S., Sanchez A.,

RA Hahey J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Toyninski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Pan Jones S.T. Marra M.A.;
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c. Natl. Acad. Sci. U.S.A.
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-!- SIMILARITY: CONTAINS 4 KH DOMAINS.

EMBL; AF064634; AAC18598.1; -.

GO; GO:0003676; F:nucleic acid binding; II

InterPro; IPR004088; KH_type_1.

InterPro; IPR004088; KH_type_1.

InterPro; IPR004088; KH_type_1.
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Pfam; PF00076; xrm; 2.
SMART; SM00322; KH; 4.
SMART; SM00360; RRM; 2.
PR0SITE; PS50084; KH TYPE 1; 4
PR0SITE; PS50102; RRM; 2.
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O1-AUG-1998 (TrEMBLrel. 07, Created)
O1-AUG-1998 (TrEMBLrel. 07, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
VG1 RNA binding protein variant D.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
NCBI TaxID=8355;
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PROSITE;
SEQUENCE
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Havin L., Git A., Elisha Z., Oberman
Pressman Schwartz S., Standart N.M.,
Genes Dev. 0:0-0(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Deshler J.O., Highett M.I., Abramson T., Schnapp B.J.; "A highly conserved RNA-binding protein for cytoplasmic mRNA localization in vertebrates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98228351; PubMed=9560341;
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GTTGTCAACGTCACATATGCAACAAGAAGAAGAAGCAAAAATAGCCATGGAGAAAGCTAAGC
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                                                              ArgLysLeuGlnIleArgAsnIleProProHisLeuGlnTrpGluValLeuAspSerLeu
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     ATCAAACAGCTGGCGAGATTCGCCGGAGCCTCTATCAAGATTGCCCCTGCGGAAGGCCCA
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EMBL; AF043253; AAB97457.1; -.
EMBL; AF064633; AAC18597.1; -.
GO; GO:0003676; F:nucleic acid binding; II
InterPro; IPR004087; KH dom.
InterPro; IPR004087; KH type_1.
InterPro; IPR004088; KH_type_1.
InterPro; IPR004084; RNA_rec_mot.
Pfam; PF00013; KH; 4.
                                                                                           Pfam: PF00076; rrm; 2.
SMART; SM00362; KH; 4.
SMART; SM00360; RRM; 2.
SMO0360; RRM; 2.
PROSITE; PS50084; KH TYPE_1; 4.
PROSITE; PS500102; RRM; 2.
PROSITE; PS000301; RRM, RNP_1; FALSE NI
SEQUENCE 593 AA; 65385 MW; 5A5AB
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"Characterization of a Xenopus oocyte
developmentally regulated cis-element
Dev. Biol. 151:306-316(1992).
                                                                                                                                                                                                                                                        Havin L., Git A., Elisha Z., Pressman Schwartz S., Standa Genes Dev. 0:0-0(1998).
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Submitted (JAN-1998)
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MEDLINE=92249652; PubMed=1577195;
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Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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-JUN-1998 (TrEMBLrel. 06, Last sequence update)
-JUN-1903 (TrEMBLrel. 25, Last annotation update)
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Zipcode-binding protein.
ROSS A.F., Oleynikov Y.S., Kislauskis E.H., Taneja K.L., Singer "Characterization of a beta-actin mRNA zipcode-binding protein." Mol. Cell. Biol. 17:2158-2165(1997).
-!- SIMILARITY: CONTAINS 4 KH DOMAINS.
EMBL; AF026527; AAB82295.1; -.
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR004087; KH_dom.
InterPro; IPR004087; KH_dom.
InterPro; IPR004087; KH_type_1.
InterPro; IPR004087; KH_type_1.
InterPro; IPR004087; KH_type_1.
InterPro; IPR004087; KH_type_1.
InterPro; IPR004087; KH_type_1.
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Eukaryota; Metazoa; Chordata;
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SMART; SM00322; KH; 4.

SMART; SM00360; RRM; 2.

PROSITE; PS50084; KH TYPE_1; 4.

PROSITE; PS50102; RRM; 2.

PROSITE; PS60030; RRM; RMP 1; FALSE NEG.

PROSITE; PS60030; RRM RMP 1; FALSE NEG.

PROSITE; PS60030; RRM RMP 1; FALSE NEG.
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STRAIN=Sprague-Dawley;
Eom T., Singer R.H., Bas
"Molecular interactions
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Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                         GCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTGATCGTCAGA
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RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RX MEDLINE=21085660; PubMed=11217851;

RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Aizawa K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Kadota K., Matsuda H.A., Ashburner M., Besole G., Quackenbush J.,

RA Kadota K., Matsuda H.A., Ashburner M., Besole G., Quackenbush J.,

RA Kahil P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Kushi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakanoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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01-OCT-2003 (TREMBLIEL. 25, Last annotation update)
Coding region determinant binding protein.
IGF2BP1 OR CRDBP.
Mus musculum for the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the 
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Mammalia; Eutheria; Rodentia;
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"Purification and properties of a protein that binds to the C-terminal coding region of human c-myc mRNA.";
J. Biol. Chem. 269:9261-9269(1994).
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"The half-life of c-myc mRNA in growing and influence of the coding and 3' untranslated ribosome translocation.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94179348; PubMed=8132663;
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MEDLINE=92217743; PubMed=1559612;
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l of c-myc mRNA half-life in vitro by a prot
to a coding region stability determinant.";
ev. 6:642-654(1992).
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Pfam; PF00013; KH; 4.
Pfam; PF00076; rrm; 2.
SMART; SM00362; KH; 4.
SMART; SM00360; RRM; 2.
PROSITE; PS50004; KH TYPE_1; 4.
PROSITE; PS50102; RRM; 2.
SEQUENCE 577 AA; 63450 MW; 1
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"ENELTY: CONTAINS 4 KH DC EMBL; AR061569, AAC72743.1; -... EMBL; AK013940; BAB29071.1; -... HSSP; P11940; ICVU.

MGD; MGI:1890357; Igf2bp1.
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                                                                                                                           CGGATCCTGGTCCCCACCCAGTTTGTTGGTGCCATCATCGGAAAGGAGGGCTTGACCATA
                              GlnGlySerProValAlaAlaGlyAlaProAlaLySGlnGlnProValAspIleProLeu
                                                                          TCCCCTTCGCCCCCAGCGAGCCCAGCGTGGGGAACCACTCTTCCCGGGAGCAAGGCCAC
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                                                                                               TTCTTTAACCCCAAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCCACA
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01-OCT-2003 (TrEMBLrel. 25,
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Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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-!- SIMILARITY; CONTAINS 4 KH DOMAINS.
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"Analysis of the mouse transcriptome based on 1
60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
EMBL; AK044850; BAC32119.1;
EMBL; AK044850; BAC32119.1;
GO; GO:0003676; F:nucleic acid binding; IEA.
InterPro; IPR004087; KH dom.
InterPro; IPR004087; KH dom.
InterPro; IPR004088; KH_type_1.
InterPro; IPR000504; RNA rec_mot.
Pfam; PF00013; KH; 4.
Pfam; PF00076; KH; 4.
SMART; SM00320; KH; 4.
SMART; SM00360; RRM; 2.
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01-MAR-2003 (TrEMBLrel. 23, I
01-OCT-2003 (TrEMBLrel. 25, I
Insulin-like growth factor 2.
IGF2BP1.
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PROSITE; PS50102; RRW; 2.
SEQUENCE 577 AA; 63378 MW;
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MEDLINE=22354683; PubMed=12466851;
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RC STRAINE-129/SV x 129/SV-CP; TISSUE-Embryonic stem cells;

RX MEDLINE-22388257; PubMed=12477932;

RX MEDLINE-22388257; PubMed=12477932;

RX Strausberg R.L., Feingold E.A., Couse L.H., Derge J.G.,

RX Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RX Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

RX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RX Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RX Altachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RX Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RX Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RX Raha S.S., Loquellano N.A., Sodergren E.J., Lu X., Gibbs R.A.,

RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RX Ryminski M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RX Rywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RX Rywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RX Rywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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01-JUN-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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    Strausberg R.;
Submitted (APR-2003)
                                       STRAIN=129/Sv x 129/Sv-CP; TISSUE=Embryonic stem cells;
                                                              SEQUENCE FROM N
                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                        Jones S.J., Marra M.A.; "Generation and initial analysis
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Pfam; PF000076; rrm; 2.
SMART; SM00322; KH; 4.
SMART; SM00360; RRM; 2.
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PROSITE; PS50084; KH TYPE_1; 4
PROSITE; PS50102; RRM; 2.
SEQUENCE 577 AA; 63378 MW;
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                                                                                             AAGAACATCACTAAGGAGACCCAGTCCCGGGTAGATATCCATAGAAAAGAGAACTCTGGA
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                               gcrecagagaagccrgrcaccarccarecareccaccacacagaggaaggaactrcrgaaagcarecec
                                                                    -GlnGlyProGluAsnGlyArgArgGlyGlyPheGlySerArgGlyGlnProArg
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RX MEDLINE=2238257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wanger L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Wanny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                 Pfam; PF00013; KH; 4.
Pfam; PF00076; rrm; 2.
SMART; SM00322; KH; 4.
SMART; SM00360; RRM; 2.
                                                                                                                                                                                                                                                     PROSITE; PS50084; KH TYPE 1;
PROSITE; PS50102; RRM; 2.
SEQUENCE
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EMBL; AP161270; AAD45610.1; --
EMBL; BC045873; AAH45873.1; --
ZFIN; ZDB-GENE-000308-1; dVII:bp
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InterPro; IPR004088; KH_type_1.
InterPro; IPR000504; RNA_rec_mot.
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                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0003676; F:nucleic
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STRAIN=AB; TISSUE=Body;
MEDLINE=22388257; PubMe
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MetAsnLysLeuTyrTleGlyAsnValSerGluGlnAlaSerAlaLeuAspLeuGluSer
                    ATGAACAAGCTTTACATCGGGAACCTGAGCCCCGCCGTCACCGCCGACGACCTCCGGCAG
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                                                                                                      AAGCCTGTCACCATCCATGCCACCCCAGAGGGGACTTCTGAAGCATGCCGCATGATTCTT
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SerAsnLeuIleProGlyLeuAsnLeuAsnAlaLeuGlyLeuPheProGlyAlaAlaSer
                                                                   AsnProGluArgThrIleThrValLysGlyThrLeuAspAlaCysAlaLysAlaGluGlu
                                                                                AACCCGGAAAGAACCATCACTGTGAAGGGCACAGTTGAGGCCTGTGCCAGTGCTGAGATA
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01-MAR-2003 (TYEMBLICEL 2
01-OCT-2003 (TYEMBLICEL 2
                                                                                                                                                                                                                              The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II
The RIKEN Genome Exploration Research Group Phase I & II
TANALYSIS of the mouse transcriptome based on functional
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
Nature 420:563-573(2002).
EMBL, AK088465; BAC40370.1; -.
Plam; r...
SMART; SM00322; KH; 4.
SMART; SM00360; RRM; 2.
SMART; PS50084; KH_TYPE_1;
                                                                                                                  MGD; MGI:1890359; Igf2bp3.
GO; GO:0003676; F:mucleic acid binding;
InterPro; IPR004087; KH dom.
InterPro; IPR004088; KH_type_1.
InterPro; IPR000504; RNA_rec_mot.
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[1]
SEQUENCE FROM N.A.
STRAIN=NOD; TISSUE=Thymus;
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Mammalia; Eutheria; Rodentia;
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                                                         Pfam; PF00013; KH; 4.
Pfam; PF00076; rrm; 2
SMART; SM00322; KH; 4
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                                                                                                                Q9CPN8 PRELIMINARY; PRT; 579 AA.
Q9CPN8;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Q1-GCT-2003 (TrEMBLrel. 25, Last annotation update)
Q1-GCT-2003 (TrEMBLrel. 25, Last annotation update)
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Q1-GCT-2003 (TREMBLrel. 17, Last sequence (IGF2 mRNA-binding (Insulin-like growth factor 2, binding protein 3).
Q1-GCT-2003 (TREMBLREL 20, MIMP3.
                    NCBI_TaxID=10090;
                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
    SEQUENCE
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Rodentia;
                                                          Craniata; Ver
Sciurognathi;
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chi; Muridae; Murinae; Mus
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PA Hayashirabi Y. Y.,
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                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones S.J., Marra M.A.; "Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                       Pfam; PF00076; rrm; 3
SMART; SM00322; KH; 4
SMART; SM00360; RRM;
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                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6; TISSUE=Brain, and Olfactory epithelium;
                                                                            Pfam; PF00013; Pfam; PF00076;
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SEQUENCE 579 AA; 63574 MW;
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Putative RNA
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                                            Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
 Oncogene
         SEQUENCE FROM N.A. Mueller-Pillasch F.,
                                   NCBI_TaxID=9606;
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NA binding protein
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                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
          Wallrapp
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EMBL; U76705; AAD09223.1; ---
GO; GO:0005737; C:cytcplasm; TAS.
GO; GO:0005737; F:RNA binding; TAS.
GO; GO:0007345; P:embryogenesis and morpho
GO; GO:0006412; P:protein biosynthesis; TA
GO; GO:0006396; P:RNA processing; TAS.
InterPro; IPR004087; KH_dom.
InterPro; IPR004087; KH_dom.
InterPro; IPR004087; KH_type_1.
InterPro; IPR0050504; RNA_rec_mot.
Pfam; PF00013; KH; 4.
Pfam; PF00016; rrm; 2.
SMART; SM00322; KH; 4.
SMART; SM00350; RRM, RNP_T; 1; 4.
PROSITE; PS50084; KH_TYPE_1; 4.
PROSITE; PS50084; KH_TYPE_1; 4.
PROSITE; PS50084; KH_TYPE_1; 4.
PROSITE; PS50084; KH_TYPE_1; AESC3A8EE3C
SEQUENCE 579 AA; 63720 MW; AESC3A8EE3C
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Mueller-Pillasch F., Lacher U., Wallrapp C.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: CONTAINS 4 KH DOMAINS.
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SEQUENCE FROM
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PheGluGln---SerGluThrGluThrValHisGlnPheIleProAlaLeuSerValGly
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                                            GCAGAAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAAAATGAGGAAGTGATCGTCAGA 1620
                                                                                        TTCTTTAACCCCAAAGAAGTGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCCTCTTCCACA
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Score:
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InterPro; IPR004088; KH_type_1.
Pfam; PF00013; KH; 4.
SMART; SM00322; KH; 4.
PROSITE; PS50084; KH_TYPE_1; 4.
SEQUENCE 580 AA; 63407 MW; 8!
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Q8IGK4;
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Eukaryota; Metazoa; Arrhropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI TaxID=7227;
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01-CCT-2003 (TrEMBLrel. 25,
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ProLeuAspArgGlnGlnLeuGluGly---
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                                                      GGGGACCACTCTTCCCGGGAGCAAGGCCACGCCCCTGGGGGCACTTCTCAGGCCAGACAG
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AsnProTyr--
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л	AACTTAACCAGTGCAGAAGTCATCGTGCCTCGTGACCAAACGCCAGATGAA	1549
1548 422	CCCTCTTCCACAGCTGGCCGGGTGATTGGCAAAGGTGGCAAGACCGTGAACGAAC	1489 403
1488 402	AAAGAGGAAAACTTCTTTAACCCCAAAGAAGAAGTGAAGCTGGAAGCGCATATCAGAGTG :::       :::::     ::    ArgGluGluGlyPheMetCysGlyThrAspAspValArgLeuThrValGluLeuLeuVal	3 2
1428 382	ATCATCACCGGGCCACCGGAAGCCCAGTTCAAGGCCCAGGGACGGATCTTTGGGAAACTG	36
1368 362	ATCAAGATTGCCCCTGCGGAAGGCCCAGACGTCAGCGAAAGGATGGTC :::	سا س
1320 3 <b>4</b> 2	GCCATCATCGGGAAGAAGGGGGCACACATCAAACAGCTGGGGAGATTCGGCGGAGGCTCT	1261 323
1260 322	TATCCAGAGCAGGAGATTGTGAATCTCTTCATCCCAACCCAGGCTGTGGGC :::	1210 303
1209 302	CCGTTCC	1189 283
1188 282	:::     :::  LeuHisP	26
1164 262	:::: ArgGlnS	24
1104 242	ACTGTGA	22
1044 222		98! 201
984 202	5 GTTGGAAGACTGATTGGAAAAGAAAGGCAGAAATTTGAAGAAAATTGAACATGAAACAGGG :::     :::     :::    :::    :::     :::     :::	· ·
924 182	3 GCCGAAGAGATTCCTCTGAAAATCTTGGCACACAATGG	• •
882 162	3 TCTGAAGCATGCCGCA:::        ::: 3 ThrAsnAlaCysLysA	
822 142	3 AAAGAGAACTCTGGAGCTGCAGAGAAGCCTGTCACCATCCAT	
122	3 GAGGGCTTGACCATA: :::        : 3 GlnGlySerThrIle:	ÖÖ
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CCCCAGGGCTTCTGCAGGCC 1997         roproglyAsnAlaThrAlaAlaAla 568	CGAGGAGGGCGGGGAAGGTCAGCCAGGTTTGCCAGAACCACCGAGCCCCGCCCTCCCGCC 1971	GAATGAGAAGTCTGCGGAGGCCGAGGACTCTGCCGAGGCCCTGAGAACCCCAGGGGC 1911	1792 CTGACAGAATGAGACCAAACGCAGCCAGCCAGATCGGGAGGAAAAGAACAAAAGACCATCTGAG 1851 :::   ::::::::::::::::::::::::::::::::	AGCAAGTGAGGCTCCCACAGGCACAGCAAAACAACGGATGAATGTAGCCCTTCCAACAC 1791	CAACAGGTGAAGCAGCAGGAGCAGAAATACCCTCAGGGAGTCGCCTCACAGCGC 1731 :::  ::::::::::::::::::::::::::::::::	AAGATCAGGGAAATTGTA 1677	:::

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